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; Search time 1486.5 Seconds (without alignments) 6298.931 Million cell updates/sec
                                                                                                                                       1 tatgaagcacggatctttac.....atccagggtgcaaatatctg 198
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                 4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
                                                                     October 22, 2004, 19:32:18
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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198
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9b htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		₩			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1 1 1 1 1		1 1 1 1 1		-		
Н	198	100.0	1588	9	AR263641	AR263641 Sequence
7	198	100.0	1659	9	E31042	E31042 Method for
m	198	100.0	1659	9	AR270490	AR270490 Semience
4	198	100.0	1659	9	HSU32974	U32974 Human IAP-1
Ŋ	198	100.0	2086	9	BC032729	BC032729 Homo sani
9	198	100.0	2404	9	CQ714226	CO714226 Segmence
7	198	100.0	2404	9	AX429575	AX429575 Segmence
œ	198	100.0	2540	9	AR103281	
6	198	100.0	2540	ø	C0789350	
10	198	100.0	2540	9	AR302736	
11	198	100.0	2540	9	AR380355	
12	198	100.0	2540	9	AR435471	
13	198	100.0	2540	9	AR451571	
14	198	100.0	2540	9	AR473581	
15	198	100.0	2540	9	AX412118	
16	198	100.0	2540	9	AX587804	
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18	198	100.0	3000	9	AR451578	AR451578 Semience
19	198	100.0	3000	9	AX412131	AX412131 Sequence

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0; Gaps

120

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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005

RESULT

121 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCTTGGGAACAACATGCTAATGGTAT

1 TAIGAAGCACGGATCTTTACTTTIGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT

6 6 6 6 6 6

Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0

180

0000000000	AF183429 Rattus no AB03336 Rattus no AF304334 Rattus no AF304333 Rattus no U36842 Mus musculu AR302739 Sequence AR43544 Sequence AR43544 Sequence AR473584 Sequence AR473584 Sequence AR412124 Sequence AR116702 Sequence AR116702 Sequence AR116702 Sequence AR116702 Sequence AR16706 Sequence AR16709 Sequence U88990 Mus musculu AC137152 Mus musculu	linear PAT 29-JAN-2003	fertility
AR106397 AR116699 BD190868 BR370617 AX670900 CQ734077 AX10456 AX104956 AC079753	AF183429 AB033346 AF304333 AF304333 AF304333 AF30736842 AR302739 AR435474 AR473584 AR473584 AR473584 AR16702 BD190871 AR370620 AK37152	ALIGNMENTS 1588 bp DNA 1t US 6331412.	ted.  1 to 1588)  G. and Lagace, M.  d compounds for modulating male is 6331412-A 3 18-DEC-2001; cocation/Qualifiers 1588 organism="unknown" mol_type="genomic DNA"
5232 5232 5232 5232 5232 1088 1752 1752	6 1491 10 6 3032 10 8 3032 10 4 2100 6 4 2100 6 4 2100 6 4 2100 6 8 2691 6	3 from patent .1 GI:28075567	Unknown. Unknown. Unclassified. Unclassified. I (bases 1 to 1588) Korneluk,R.G. and Lagace,M. Methods and compounds for mo Patent: US 6331412-A 3 18-DE Location/Qualifiers 1. 1588 /organism="unknown" /mol_type="genomic.
100 100 100 100 100 91 91	179.4 90. 179.4 90. 177.8 89. 173. 87. 173. 87. 173. 87. 173. 87. 169.8 85. 169.8 85. 169.8 85.	AR263641 Sequence AR263641 AR263641	Σ υ
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	и чи	RESULT 1 ARZ63641 LOCUS DEFINITION ACCESSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOHNAL FEATURES SOURCE

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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1659)

1 (bases 1 to 1659)

1 Ubases 1. O 1659,

2 (Brillan, R.C., Nava, V.B., Gedrich, R.W., Clem, R.J., Van Dongen, J.L., Gilfillan, M.C., Shiels, H., Hardwick, J.M. and Thompson, C.B.

A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors

EMBO J. 15 (11), 2685-2694 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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YSVNKEQLARAGFYALGBGDKVKCFHCGGGLTDWKPSEDPMEQHAKWYPGCKYLLEQK
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Duckett, C.S. and Thompson, C.B.
Direct Submission
Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60657, USA
Location/Qualifiers
                                                                                                                                  Length 1659;
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Human IAP-like protein ILP mRNA, complete cds.
U32974
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100.0%; Score 198; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;
Matches 198; Conservative 0; Mismatches 0;
Patent: US 6500938-A 1053 31-DEC-2002;
Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="heart"
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                                                 /organism="unknown"
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32. .1575
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                   E31042 110ear PAT 18-JUN-2001 Method for screening substance inhibiting binding to XIAP.
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Unclassified.
I (bases 1 to 1659)
Au-Young,J. and Seilhamer,J.J.
Composition for the detection of signaling pathway gene expression
                                                                                                                                                                                                                                                                 OS Unidentified
PD JP9932628-A/2
PD 26-NOV-1999
PF 13-MAY-1999 JP 1998130378
PR KUNHIRO MATSUMOTO
PC GOIN33/566,A6IK38/00,A6IK38/00,A6IK38/00,A6IK38/22,
PC A6IX59/395,
PC A6IX55/00,A6IK45/00,A6IK45/00,C07K7/06,C07K7/08,C07K14/47, PC GOIN33/536,
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G01N33/536,G01N33/536//C12N15/09,C12P21/08,A61K37/02,A61K37/02,PC
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larity 100.0%; Pred. No. 2.8e-44;
Conservative 0; Mismatches 0;
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AR270490
AR270490.1 GI:29701724
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Strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .1659
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Topology: Linear;
Key L
                                                                           E31042.1 GI:13017307
JP 1999326328-A/2.
unidentified
                                                                                                                                                        unclassified.
1 (bases 1 to 1659)
Kunihiro,M.
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Best Local Similarity
Matches 198; Conserv
                                                                                                                                      unidentified
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PC A61K37
CC Strand
CC Topolo
FH Key
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PRI 12-JUN-1996

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Sites http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Rhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho.S.-L., Karline,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 69 Row: j Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502142.
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YSEBARLKSFQNWPDYAHLTPRELASAGLYYTGIGDOVQCFCCGGKLKNWEPCDRAWS
BHRRHFPNCFFVLGRNLNIRSESDAVSSDRNFPNSTNLPRNPSMADYBARIFTFGTWI
YSVNKEQLARAGFYALGBGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQK
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MEEKIQISGSNYKSLEVLVADLVNAQKDSMQDESSQTSLQKEISTEEGLRRLQEEKLC
KICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS"
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="baculoviral IAP repeat-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="synonyms: MIHA, ILP1, API3, XIAP"
'db_xref="LocusID:331"
'db_xref="MIM:300079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Uterus, leiomyosarcoma"/clone_lib="NIH_MGC_71"
                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="MGC:45369 IMAGE:5532247"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAH32729.1"
db_xref="G1:21619764"
db_xref="LocusID:331"
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                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .2086
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/codon_start=1
                                                                                                                                       Contact: MGC help desk
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Klaushery, R.L., Zeeberg, B., Buetow, K.H., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Jordan, H., Morce, T., Mans, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, Y., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jonnes, S.J. and Marra, M.A.
                            MEEKIQISGSNYKSLEVLVADLVNAQKDSMPDESSQTŠIQKEISTEEQLRRLQEEKL.
KICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVITFKQKIFMS"
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Homo sapiens baculoviral IAP repeat-containing 4, mRNA (cDNA clone
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2086)
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               874 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                      1420. .1542
/note="RING finger"
                                                                                                                                                    574. .774
/note="IAP repeat"
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                                                                                                                    /note="IAP repeat"
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Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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REFERENCE
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BC032729
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACAACATGCTAAATGGTAT 1005
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                                                                                                                                                                                                                                         827 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Unclassified.

(Dases 1 to 2540)

Bennett, C.Frank, Ackermann, E.J. and Cowsert, L.M.
Antisense modulation of X-linked inhibitor of apoptosis
Patent: US 6087173-A 1 11-JUL-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2540;
                                                                                                                            Length 2404;
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                100.0%; Score 198; DB 6;
100.0%; Pred. No. 2.7e-44;
iive 0; Mismatches 0;
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Location/Qualifiers
1. 2404
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR103281 2540 bp
Sequence 1 from patent US 6087173.
AR103281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGGTGCAAATATCTG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                         181 CCAGGGTGCAATATCTG 198
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                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 198; Conservative
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CQ789350
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ORGANISM
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 198; Conservative 0; Mismatches 0; Indels 0
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Patent: WO 02068579-A 160 06-SEP-2002;
PE Corporation (NY) (US)
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/db xref="taxon:9606"
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/organism="Homo sapiens"
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/mol_type="genomic DNA'
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                                                                                                                                      Kroenke, M., Kashkar, H., Hamilton-Dutoit, S.J. and Juergensmeier, J.M. USE OF IAP FOR THE DIAGNOSIS AND OF IAP-INHIBITORS FOR THE TEATHENT OF HODGKINÆRSQUO, S. IYMPHOMAS PATENT WO 2004017991-A 1 04-PARA-2004;
Cell Center Cologne GmbH (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Korneluk, R.G., MacKenzie, A.E., Baird, S. and Liston, P.
Mammalian IAP gene family, primers, probes and detection methods
Patent: US 6541457-A 3 01-APR-2003;
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="GI:45822922"
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Cocks.B.G., Stuart,S.G. and Seilhamer,J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 900 19-AUG-2003;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-44;
Matches 198; Conservative 0; Mismatches 0;
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Sequence 900 from patent US 6607879.
AR380355.1 GI:40087989
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946 GGAGGCTAACTGAITGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              1 (bases 1 to 2540)
Korneluk,R.G., MacKenzie,A.E., Baird,S. and Liston,P.
Mammalian IAP gene family, primers, probes and detection methods
Patent: US 6689562-A 3 10-FEB-2004;
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Patent: WO 0226956-A 218 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
Location/Qualifiers
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larity 100.0%; Pred. No. 2.7e-44;
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AX412118

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from patent US 6689562.
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1006 CCAGGGTGCAAATATCTG 1023
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Sequence 3 from patent 0
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AR473581.1 GI:42711906
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                                                     1 (bases 1 to 2540)
Korneluk, R.G., MacKenzie, A.E., Baird, S. and Liston, P.
Mammalian apoptosis inhibitor protein gene family, primers, probes
and detection methods
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Krorneluk, R.G., LaCasse, E., Baird, S., Holcik, M. and Young, S.
Antisense Incleic acids and uses thereof
Patent: US 6673917-A 218 06-JAN-2004;
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Sequence 218 from patent US 6673917.
AR451571
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AR451571
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Search completed: October 22, 2004, 21:14:31 Job time : 1489.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

October 22, 2004, 19:31:13 ; Search time 261 Seconds (without alignments) 3982.319 Million cell updates/sec Run on:

US-09-654-743-47 Perfect score: Title:

1 tatgaagcacggatctttac.....atccagggtgcaaatatctg IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

198

4134886 segs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn2001as:\*
geneseqn2001bs:\*
geneseqn2002as:\*
geneseqn2002bs:\* geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2003as:\*
geneseqn2003bs:\* N\_Geneseq\_23Sep04:\* genesegn1980s:\*
genesegn1990s:\*
genesegn2000s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:\*

SUMMARIES

	Description	Abs52803 DNA encod	Aaz48862 Human XTA	Aca56455 Human sig	Adi56251 Human pol	Aak99405 DNA of AP				Abv94283 Breast Ca	Aal53731 X-linked	Aad49663 Human X-1	Adb81002 RING-SH C	Adg89383 Cancer de	Adi31574 Human CDN	Adh74638 DNA encod	Adl70165 Human X c	Abk93875 Human cDN	Aav55038 Human XIA	Himan	Monga	Mouse	•
	ID	ABS52803	AAZ48862	ACA56455	ADI56251	AAK99405	AAT70836	AAA64901	ABK93869	ABV94283	AAL53731	AAD49663	ADB81002	ADG89383	ADI31574	ADH74638	ADL70165	ABK93875	AAV55038	AAD03575	AAT72710	AAT70839	
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<b>₩</b>	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.1	88.2	87.4	
	Score	198	198	198	198	198	198	198	198	198	198	198	198	198	198	198	198	198	198	180.4	174.6	173	
	Result No.	-	7	Э	4	Ŋ	y	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	

Abk93872 Mouse CDN				Abk14678 Human Inh	Abk14677 Human Inh	Aad03581 Human IAP	Aaa06940 DNA encod	Abk13197 Human tes	Abs52802 DNA encod	Aad03583 Gorilla I			Human	Human	CDNA	Adb80989 RING-SH C	Aca56478 Human sig	Adi31568 Human cDN	Adi56274 Human pol	Aat61591 Human c-I	Aat70837 Human abo	Abk93870 Human cDN	Adf45449 Human vas
ABK93872	AAV55041	ABZ58102	AAD03582	ABK14678	ABK14677	AAD03581	AAA06940	ABK13197	ABS52802	AAD03583	AAX02960	AAX03018	ABQ58785	AAX03028	AD026591	ADB80989	ACA56478	ADI31568	ADI56274	AAT61591	AAT70837	ABK93870	ADF45449
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2100	2691	2691	711	1758	1758	4993	711	1559	1559	711	578	802	302	1402	1448	2563	2563	2563	2563	2601	2666	2676	2916
87.4	85.8	85.8	83.8	83.8	83.8	83.8	83.0	83.0	83.0	82.2	79.7	66.4	48.9	41.9	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7
173	169.8	169.8	166	166	166	166	164.4	164.4	164.4	162.8	157.8	131.4	8.96	83	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6
22	23	24	25	56	27	28	29		31	32	c 33	34	c 32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Inhibitor of apoptosis protein, IAP; testis; XIAP; apoptosis; TIAP; fertility; testicular cancer; male infertility; male birth control; X-linked inhibitor of apoptosis; gene; ds.
                                                                                                                                                  /note= "Start codon illegible in specification; represented as nnn"
                                                     DNA encoding X-linked inhibitor of apoptosis, XIAP.
                                                                                                           Location/Qualifiers
               BP.
              ABS52803 standard; DNA; 1588
                                        (first entry)
                                                                                                                                              partial
                                        15-NOV-2002
                                                                                               Mammalia.
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/\*tag= a /transl\_except= (pos:34. .36, aa:Xaa) /product= "X-linked inhibitor of apoptosis protein, XIAP"

US2002086409-A1.

04-JUL-2002.

18-DEC-2001; 2001US-00024433

29-JAN-1998; 98US-0073001P. 29-JAN-1999; 99US-00239867.

(KORN/) KORNELUK R G. (LAGA/) LAGACE M.

Korneluk RG, Lagace

WPI; 2002-642245/69. P-PSDB; ABG32418.

Novel polypeptide, a member of inhibitor of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells,

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Disclosure; Page 28-30; 43pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                994
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                                                                                                                                                                                                               Query Match
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                                           A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of apoptosis) family of proteins that is expressed in the testes. (I) is apoptosis of inclination of apoptosis and accompound that modulates TIAP biological activity (I) is useful for increasing apoptosis in a cell, preferably a germ-line cell and for increasing fertility in an animal. (I) is useful for treating apoptosis which occurs as a part of testicular cancer and male infertility. TIAP may be manipulated for use as a male birth control. TIAP polypeptides and nucleic acid sequences also have abarrant levels of apoptosis. The present sequence represents the coding sequence of X-linked inhibitor of apoptosis (XIAP)
                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, TAB1, XIAP, X-linked inhibitor of apoptosis protein, TGF-beta, transforming growth factor-beta activated kinase 1; monocyte migration, TAK1 binding protein 1; extracellular matrix protein production, cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta; ds.
                                                                                                                                                                                                                                                                                    826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                     886 GCAAGAGCTGGATTTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
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                                                                                                                                                                                                                                                                                                             GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
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                                                                                                                                                                                                               Length 1588;
                                                                                                                                                                                          Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                100.0%; Score 198; DB 6; 100.0%; Pred. No. 3.8e-54;
 particular cells involved in male fertility.
                                                                                                                                                                                                                                      0; Mismatches
                       Example 3; Fig 4A; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGGTGCAAATATCTG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human XIAP coding sequence.
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                           Local Similarity
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                method for screening a substance inhibiting the formation of a complex between XIAP and TABI, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase I (TAKI) binding protein 1 (TABI) and a substance to be tested are contacted with each other and then the presence to formation of a complex between XIAP and TABI is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TABI and XIAP as well as between XIAP and TGF-beta (Transforming growth factor-beta) type I and/or type II receptor is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; probe; ss; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 198; DB 3; 100.0%; Pred. No. 3.9e-54;
sequence encodes the human XIAP protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seilhamer JJ;
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Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    useful as a drug
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New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic

98US-00016434.

30-JAN-1998;

(INCY-) INCYTE GENOMICS INC.

33;

Au-Young J,

WPI; 2004-090520/09.

fragments.

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                           The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnostics and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, correctly and paramacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding carray can detect changes in expression in a large number of genes coding various diseases including cancer e.g. adenocarcinoma and leukaemia.

Immunopathies e.g. AIDS and aschma, neuropathies e.g. Alzheimer's disease including cancer e.g. adenocarcinoma and leukaemia.

Immunopathies e.g. AIDS and aschma, neuropathies e.g. Alzheimer's disease to brobe of the invention. Note: The sequence data for this patent did not formal directly from USPTO at the printed specification but was obtained in electronic format directly the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994 GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cerrix; tumour; immunopathology; AlDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 198; DB 10; Length 1659; 100.0%; Pred. No. 3.9e-54; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocID=06500938B1
Claim 1; SEQ ID NO 1053; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 198; Conservative
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26-NOV-2002; 2002US-00305720.

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The invention relates to a composition of polynuclectide probes comprising itst polynuclectide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynuclectide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the polypeptide and third polynuclectide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynuclectides. The microarray is useful in the camposition are useful as array elements in a microarray for monitoring the expression of target polynuclectides. The microarray is useful in the neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or plarmacogenomics. That may be associated with the altered expression of diseases that may be associated with the altered expression of diseases that may be associated with the altered expression of gignalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, cDNAs, cDNAs, cDNAs, cDNAs, cDNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, hone marrow, brain, breast or cervix, culcarative colitis, or a neuropathology, e.g. dementia, annessia, epilepsy, Alzheimer's disease or depression. This sequence represents a human polynucleotide proper of the invention. Note: The sequence data for this parent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA of APP related human homologue hCP35211.
Claim 6; SEQ ID NO 1053; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV;

Human apoptosis inhibitor xiap cDNA.

02-SEP-1997

AAT70836;

AAT70836 standard; cDNA; 2540 BP

RESULT 6

AAT70836

AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis; ds.

Location/Qualifiers 34. .1527 /\*tag= a

Homo sapiens

myocardial

WO9706255-A2

96WO-IB001022 95US-00511485 95US-00576956

05-AUG-1996;

04-AUG-1995; 22-DEC-1995;

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The invention relates to a transgenic fly whose genome comprises DNA percoding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence encodes a 123 (Abeta42) amino acid sequence. The DNA sequence is operably linked to a tissuespecific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonuclectide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynuclectide sequence represents the DNA of the APP related human homologue hCP35211
Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Protein of human homologue hCP35211"
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Freuler F, Konsolaki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finelli AL,
                                                                                                                                                                                                                                                                       Location/Qualifiers
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14-JUN-2001; 2001US-0298309P.
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Reinhardt MWHM, Zusman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-315796/35.
P-PSDB; AAO20511.
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Liston

Baird S,

Mackenzie AE,

Korneluk RG,

(UYOT-) UNIV OTTAWA

WPI; 1997-154262/14.

P-PSDB; AAW19581

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAAGAGCTGGATTTTATGCTTTAGGTGAAGATGATAAAGTAAAAGTGAAAAGTGATGTGTGGGA 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGGCTAACTGGAATGGCCCAGTGAAGACCCTTGGGAACAACAACATGCTAAATGGTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding an inhibitor of apoptosis polypeptide - used inhibit apoptosis in e.g. HIV or AIDS patients, and for detection osusceptibility to apoptotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and disorders involving apoptosis (anti-apoptotic gene therapy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 198; DB 2;
Pred. No. 4.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 67-68; 219pp; English
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Best Local Similarity
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181

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1007 ccadedrecaaararcre 1024 CCAGGGTGCAAATATCTG 198

120 886

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Gaps . 0

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100.0%; Score 198; 100.0%; Pred. No. 4

Best Local Similarity 100. Matches 198; Conservative

à g

Query Match

; DB 6; Length 2404; 4.4e-54;

1 TAIGAAGCACGGAICTITACTITIGGGACAIGGAIAIACICAGITAACAAGGAGCAGCTI 827 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA GGAGGGCTAACTGGTTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT

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The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPI or HIAPI. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of enhancing apoptosis in a cell, comprising administering a negative regularor of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, subtain or prevent proliferative diseases (e.g. ovarian cancer.) adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or continuous where apoptosis is involved or implicated (e.g. embryonic
                         946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAATGGTAT 1005
     GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCCTTGGGAACAACATGCTAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative diseases.
                                                                                                                                                                                                                                                                                                                                         Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 198; DB 6; Length 2540; 100.0%; Pred. No. 4.5e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young
                                                                                                                                                                                                                                                                                                      Human cDNA encoding inhibitor of apoptosis, XIAP #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holcik M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baird S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 135pp; English.
                                                                                                                                                                                                   ABK93869 standard; cDNA; 2540 BP.
                                                                                                          1006 ccadedrecaaararcre 1023
                                                                           181 CCAGGGTGCAAATATCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AEGE-) AEGERA THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00672717.
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                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-479562/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200226968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korneluk RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000;
                                                                                                                                                                                                                                                                       26-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2002
     121
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                                                                                                                                                            RESULT 8
ABK93869
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                                                                                                                                                                                                                  임
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to antisense oligonucleotides designed to inhibit expression of the human X-linked inhibitor of apoptosis. The present sequence is the X-linked inhibitor of apoptosis DNA, Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are more effective inhibitors than unmodified oligonucleotides. The oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis expression in cells and tissues in vtro. The oligonucleotides are also useful for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to prevent infection, inflammation or tumour formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense compound useful for research reagents, diagnostics, prophylaxis and for treating disorders associated with X-linked inhibitor of apoptosis, modulates expression of X-linked inhibitor of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                                                                                                                   X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "X-linked inhibitor of apoptosis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 198; DB 3;
100.0%; Pred. No. 4.5e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                Human X-linked inhibitor of apoptosis DNA.
                                                                                                                                                                                                                                                                                                                       antiinflammatory; cytostatic; tumour; ds
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                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                     1006 CCAGGGTGCAAATATCTG 1023
                                                                                                                                                            BP.
                                   181 CCAGGGTGCAAATATCTG 198
                                                                                                                                                          AAA64901 standard; DNA; 2540
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                                                                                                                                                                                                                                07-NOV-2000
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differentiating a tumour with lymph nodes
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(I) have cytostatic activities and can be used as anti-tumour agents. (I) is useful in molecular characterisation of a carcinoma. (I) are cuseful for the prognosis or diagnostic of tumour, in differentiating a normal cell from a cancer cell, detecting a hormone sensitive tumour
                                                                                                                                           946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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                                                                                                                                                                                                                                                                                                                                                                          breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
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                                                                           61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
                                                                                           886 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
                                                                                                                             GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT
                                                826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                         1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
Gaps
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Mismatches
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                                                                                                                                                                                                                                                                   ABV94283 standard; cDNA; 2540
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lymph nodes, differentiating antracycline-sensitive tumours from antracycline-insensitive tumours, and classifying good and poor prognosis primary breast tumours. (I) is useful for large-scale molecular characterisation of breast cancer that help in prediction, prognosis and cancer treatment, and for detecting differentially expressed genes that correlated with a cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                              Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 198; Conservative
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAATGGTAT 1005
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   complex by mass spectrometry. The method is useful for high-throughput screening of libraries of compounds to identify pharmaceutical leads. This polynucleotide sequence represents one of the target RNA motifs/
                                                                                                                                                                                                                                 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                            100.0%; Score 198; DB 8; 100.0%; Pred. No. 4.5e-54;
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Matches 198; Conservative
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AAD49663 standard; DNA; 2540 BP. RESULT 11

24-MAR-2003 AAD49663;

Human X-linked inhibitor of apoptosis protein (XIAP) DNA

Amyloidosis; haemophilia, Alzheimer's disease; atherosclerosis; cancer; gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis; autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic; neurodegenerative disorder; parkinson's disease; gene therapy; virucide; haemostatic; antibacterial; nootropic; neuroprotective; cytostatic; XIAP; fungicide; human; X-linked inhibitor of apoptosis protein; gene; ds. 

Homo sapiens

WO200283953-A1

24-OCT-2002

11-APR-2002; 2002WO-US011757.

11-APR-2001; 2001US-0282965P

(PTCT-) PTC THERAPEUTICS INC.

Welch E; Rando R, WPI; 2003-075561/07.

Identifying a test compound that binds to a target RNA molecule for treating or preventing amyloidosis, hemophilia, cancer, gigantism, diabetes, by contacting a detectably labeled target RNA molecule with a test compounds library of

Example; Page 88-89; 152pp; English.

The invention relates to a method for identifying a test compound that binds to a target RNA molecule, which comprises contacting a detectably labelled target RNA molecule with a library of test compounds under conditions that permit direct binding of the labelled target RNA to a member of the library of test compounds so that a detectably labeled

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target RNA:test compound complex is formed. The method is useful for screening libraries of compounds for those that are selectively bind to a pre-selected target RNA. The compounds are useful for inhibiting the formation of a specific bound RNA:host cell factor complexes in vivo. They are also useful for treating or preventing diseases associated with overproduction or decreased protein function, such as amyloidosis, haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism, dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging, inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative disorders, Parkinson's disease or infections (bacterial, viral, fungal). The invention is also used in gene therapy. The present sequence is human X-linked inhibitor of apoptosis protein (XIAP) DNA. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses,
                                                                                                                                                                                                                                                                                                                                                                                                                      826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Disclosure; SEQ ID NO 331; 198pp; English.
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ADI31574
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                                                                                                                                                                                                                                                                                                                                                                                         946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
                                             The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, P13K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, WHS-UHM, a GTPase, an E2 enzyme, tsg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for identifying agents having antivixra activity, and for treating viral disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting clinical outcome for a patient diagnosed with cancer comprises determining the expression level of one or more genes, and compared to the amount found in a reference cancer tissue set.
                                                                                                                                                               polynucleotide represents a DNA sequence relating to a protein comprising
                                                                                                                                                                                                                                                                                                  882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; cancer; gene expression;
estrogen receptor-positive invasive breast cancer.
                                                                                                                                                                                                                         Score 198; DB 9;
Pred. No. 4.5e-54;
0; Mismatches 0;
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                                                                                                                                                                         the RING-SH complex of the invention.
                        Disclosure; Fig 75; 176pp; English.
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                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 198; Conservative 0
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18-SEP-2002; 2002US-0412049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOMIC HEALTH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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The invention relates to a method of predicting clinical outcome for a patient diagnosed with cancer by determining the expression level of one or more genes, or their expression products, sealected from p53B22, cathepsin B, cathepsin L, Ki67/MiB1, and thymidine Kinase in a cancer tissue obtained from the patient, normalized against control gene(s), and compared to the amount found in a reference cancer tissue set. The specification also discloses an array comprising polynuclecides (bybridizing to the following genes: FOXMI, PRAME, B612, STKIS, CEGFI, Ki-CT GSTMI, CA9, PR, BBC3, NMEI, STW, GATA3, TFRC, YB-1, DFYD, GSTM3, RPS6KB1, Sro, ChNI, IDI, ESKHI, p27, CCNBI, XIAP, CHK2, CDC25B, IGFIR, AXO55699, PI3XC2A, TGFB3, BAG11, CYP3A4, BCPCAM, VEGFC, p52, HBW1, TFSI, HSPP1, HTRIA, IGFBP3, CTSB, HAPZ and DIABHO, immobilized on a solid surface. The methods are useful for predicting clinical outcome for a patient diagnosed with invasive breast cancer on with estrogen receptor (ER) clinelihood of long-term survival of a breast cancer or with estrogen receptor (ER) clinelihood of long-term survival of a breast cancer or with estrogen receptor (ER) clinelihood of long-term survival of a breast cancer or with estrogen receptor (ER) clinelihood of long-term survival of a breast cancer or with estrogen receptor (ER) constitute invasive breast cancer or with estrogen receptor (ER) constitute invasive breast cancer or with estrogen receptor (ER) constitute invasive breast cancer or with estrogen receptor (ER) constitute invasive breast cancer or with estrogen receptor (ER)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected thybridisation complexes with the level of hybridisation complexes or relates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs the diagnosis of an immunopathology, such as Crohn's disease, asthma, contentifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAS, cDNAS or invention Note. The sequence represents a human cDNA of them
                                                                                                      A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ention. Note: The sequence data for this patent did not form part of printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 900; 50pp; English
  Seilhamer JJ;
  Stuart SG,
                                                      WPI; 2003-895307/82
                                                                                                                                                                                               or osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
Cocks BG,
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Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other; Query Match

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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005
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                                                                                                         TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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100.0%; Score 198; DB 11; Length 2540; 100.0%; Pred. No. 4.5e-54; ive 0; Mismatches 0; Indels 0;
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               Best Local Similarity 100.
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ADH74638 standard; DNA; 2540 

ADH74638;

15-APR-2004

DNA encoding human XIAP.

Biomarker; prostate neoplastic condition; inhibitor of apoptosis; IAP;

946 GGAGGGCTAACTGATGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005 The present invention relates to a method for identifying a biomarker that is diagnostic for the survival of patient with a prostate neoplastic condition. The method comprises measuring the level of inhibitor of apoptosis (IAP) polypeptide chosen from chosen from XIAP (X chromosomelinked inhibitor of apoptosis), clap1 and clAP2 in a neoplastic prostate cell-containing sample from patients, and identifying correlation between the level of IAPs in the sample, where the correlation of an IAP with survival in the patients indicates IAP as a biomarker diagnostic. The method is useful for the prognosis of prostate neoplastic conditions such as prostate cancer. The method is efficient in determining the prognosis 120 180 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 885 09 Identifying biomarker that is diagnostic for survival of a patient with prostate neoplastic condition by measuring level of integrin associated protein in sample, and identifying correlation of the level in sample. GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 121 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA while the patient is still at an early stage of disease, and in monitoring the effectiveness of a particular treatment in a prostate neoplastic condition. The present sequence encodes human XIAP. Gaps XIAP; X chromosome-linked inhibitor of apoptosis; cIAP1; cIAP2; prostate cancer; human; gene; ds. 0 100.0%; Score 198; DB 12; Length 2540; 100.0%; Pred. No. 4.5e-54; ive 0; Mismatches 0; Indels 0; Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other; Disclosure; SEQ ID NO 1; 42pp; English. 1006 CCAGGGTGCAAATATCTG 1023 181 CCAGGGTGCAAATATCTG 198 .2-FEB-2003; 2003US-00366307 12-FEB-2002; 2002US-0356956P Best Local Similarity 100. Matches 198; Conservative Krajewski S; 2004-141816/14. REED/) REED J C. KRAJ/) KRAJEWSKI P-PSDB; ADH74639 US2003224399-A1 Homo sapiens. 04-DEC-2003. JC, Query Match 61 Reed 8 셤 à g ð g à 셤

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Search completed: October 22, 2004, 20:24:53 Job time : 264 secs

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OM nucleic - nucleic search, using sw model

October 22, 2004, 20:15:23 Run on:

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US-09-654-743-47

198 1 tatgaagcacggatctttac.....atccagggtgcaaatatctg score: Sequence: Title: Perfect :

Scoring table:

824507 seqs, 355394441 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

1649014 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* Issued Patents NA:\* 4 2 6 4 5 9 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3. Appli	o m	101	, m	Sequence 1, Appli	'n		m		3	7	m	m	m	0		0	224	6	Sequence 9, Appli	6	6	Sequence 3, Appli	'n	-	ì	Sequence 16, Appl
SUMMARIES	ID	US-09-239-867-3	-10-	US-09-016-434-1053	-08-511-485-3	-58	-09-201	-09-023-65	-09-011	-60-	-60	-60-	US-09-212-971-3	-80	-09-617-	US-08-511-485-9	-09-201-936-	-09-011	US-09-672-717-224	-09-201-	-09-212-	US-08-800-929A-9	US-09-617-053A-9	US-09-121-979-3	-31	US-09-239-867-1	4	US-09-128-155-16
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	Length	1588	1588	1659	2540	2540	2540	2540	2540	2540	2540	3000	5232	5232	5232	2100	2100	2100	2100	2100	2691	2691	2691	711	711	1559	55	152331
οķο	Query	100.			100.0		100.		100												v.		ď.	Э.	e,	۳.	83.0	•
	Score	198	198	198	198	198	198	198	198	198	198	198	198	198	198	173	173	173	173	173	φ,	g)	169.8	164.4	164.4	164.4	164.4	157.8
	Result No.	Н	73	m	4	Ŋ	ø	7	æ	9	10	11	12	13	14	15	16	17	18	19	20			23				c 27

Seguence 17. Appl	Seguence 57, Appl	1076	-		m	Ŋ	'n	, Lo	220	5	31.	1.7	1	7. A	ις.	'n	2
US-09-128-155-17	US-09-579-692B-57	US-09-016-434-1076	US-09-023-655-894	US-08-569-749-3	PCT-US96-12860-3	US-08-511-485-5	US-09-201-936-5	US-09-011-356-5	US-09-672-717-220	US-09-201-932-5	US-09-814-915A-31	US-09-205-144-1	US-09-814-915A-11	US-09-579-692B-7	US-09-212-971-5	US-08-800-929A-5	US-09-617-053A-5
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176373	1448	2563	2563	2601	2601	2676	2676	2676	2676	2676	2916	3076	3076	3734	6999	6999	6999
66.4	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7
131.4	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6
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## ALIGNMENTS

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           ; Sequence 3, Application US/09239867; Patent No. 6313142; GENERAL INFORMATION:
; APPLICANT ROBERT G. KORNELUK et al.; APPLICANT ROBERT G. KORNELUK ET ITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FABLESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 198; DB 3; Best Local Similarity 100.0%; Pred. No. 1.9e-59; Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             LENGTH: 1588
US-09-239-867-3
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121 GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180 826 TATGAAGCACGGATCTTTACTTTTGGGACATGATACTCAGTTAACAAGGACAGCTT 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTGCTTTTCACTGTGGA Sequence 3, Application US/10024433
; Patent No. 6797473
; GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILLITY CCAGGGTGCAATATCTG 1023 181 CCAGGGTGCAAATATCTG 198 RESULT 2 US-10-024-433-3 1006 g ð

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Boston
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US-08-511-485-3
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US-08-511-485-3
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                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                         Length 1588;
                                                                                                                                                                                                                                                                                                                  Indels
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 198; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/10/024,433
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/239,867
PRIOR FILING DATE: 1999-01-29
                                                                                                      NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1006 ccaddargcaaararcrd 1023
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TELEFAX: 050 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                              SEQ ID NO 3
LENGTH: 1588
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-016-434-1053
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994 ggaggerraacrearregaagcecagreaagacecrreggaacaacareargraarregrar 1053
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                                                                                                                                                                                                                                                                                                                                                 1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                   100.0%; Score 198; DB 4; Length 1659; 100.0%; Pred. No. 1.9e-59; or Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08511485
Patent No. 5919912
Patent Normalion:
Papelicant: Mackenzie, Alexander E.
APPLICANT: Markenzie, Alexander E.
APPLICANT: Marid, Stephen
ITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMER TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1054 ccadedrecaararcre 1071
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TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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TELERAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
1659 base pairs
                                                                                                                                                                                                                                                                                               Matches 198; Conservative
                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                           ; TOPOLOGY: linear; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 91016687
US-09-016-434-1053
                                                                                                                                                                                                                                                                     Best Local Similarity
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STRANDEDNESS:
TOPOLOGY: both
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946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT
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APPLICANT: Cocks, Benjamin G.

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTTCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2540;
     TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07991/003003
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: PCT/1896/01022
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
NUMBER OF SEQ ID NOS: 45
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
MUMBER OF SEQ ID NOS: 45
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COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.fre
FILING DATE: HERRWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 198; DB 4;
100.0%; Pred. No. 2.3e-59;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (2540) ... (2540)
CTHER INFORMATION: N may be any nucleotide US-09-201-936-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 900, Application US/09023655; Patent No. 6607879
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Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: PALO ALT
STATE: CALIFOR
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-023-655-900
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APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIC
FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                  946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACAACATGCTAAATGGTAT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
                                                                                                                                                                                                                           61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
                                                                                                                                                                                                                                                                               886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGTGA 945
                                                                                                                                                       GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
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                                                                      Gaps
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     Length 2540;
                                                                0; Indels
Query Match
100.0%; Score 198; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0;
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US-09-201-936-3
; Sequence 3, Application US/09201936
; Patent No. 6541457
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
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ORGANISM: Homo sapiens
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; LOCATION: (34)..(1527)
US-09-392-580-1
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Best Local Simi
Matches 198;
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US-09-392-580-1
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                                                                         Length 2540;
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                                                                      100.0%; Score 198; DB 4;
100.0%; Pred. No. 2.3e-59;
tive 0; Mismatches 0;
OTHER INFORMATION: N may be any nucleotide
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LOCATION: (1)...(2540)
OTHER INFORMATION: n=a,t,c, or g
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APPLICANT: Korneluk, Robert
                                                                         Query Match
Best Local Similarity 100.
Matches 198; Conservative
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US-09-672-717-218
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        ; OTHER INFORM
US-09-011-356-3
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100.0%; Score 198; DB 4; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0
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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Maid Stephen
APPLICANT: Liston, Peter
TILE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07981/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT FILING DATE: 1998-09-14
EARLIER FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENGATION INFORMATION:
TELEPHONE: (650) 855-655
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 855-655
TELEFAX: (650) 855-4166
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STRANDEDNESS: single
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ORGANISM: Homo sapiens
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CLONE: 91184319
US-09-023-655-900
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US-09-011-356-3
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
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i LOCATION: (4622)
i COTHER INFORMATION: n can be any nucleotide
VS-09-212-971-3
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                ; ORGANISM: Homo sapiens
US-09-672-717-231
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APPLICANT: Korneluk, Robert G.
APPLICANT: Lacasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Boird, Stephen
APPLICANT: Woung, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025001
CURRENT APPLICATION UNMER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 3000
Sequence 3. Application US/09201932A

Patent No. 6689562
GENERAL INFORMATION:
APPLICANT: MacKenzie, Alexander B.
APPLICANT: MacKenzie, Alexander B.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
CURRENT APPLICANTON NUMBER: 09/01,932A
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 08/51,956
EARLIER APPLICATION NUMBER: 08/51,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 198; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 198; Conservative 0; Mismatches 0;
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NAME/KEY: variation
NAME/KEY: variation
NAME/KEY: (2540)
OTHER INFORMATION: N may be any nucleotide
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; Sequence 231, Application US/09672717
; Patent No. 6673917
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Parat, Christine
ITILE OF INVENTION: DETECTION AND MODULATION OF LAPS AND
ITILE OF INVENTION: DISEASE
ITILE OF INVENTION: DISEASE
FILE REFERENCE: 07891/00902
CURRENT APPLICATION NUMBER: US/09/212,971B
FILE REFERENCE: 07891/00902
CURRENT APPLICATION NUMBER: 60/010,354
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1996-04-26
EARLIER FILING DATE: 1996-011-14
EARLIER FILING DATE: 1996-01-11-14
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FEASESQ for Windows Version 4.0
ILENGTH: 6323
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Query Match 100.0%; Score 198; DB 4; Length 3000; Best Local Similarity 100.0%; Pred. No. 2.5e-59; Matches 198; Conservative 0; Mismatches 0; Indels 0
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Sequence 3, Application US/09617053A

Sequence 3, Application US/09617053A

Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: Liston, Peter

APPLICANT: Bard, Stephen

APPLICANT: Pratt, Christine

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

TITLE OF INVENTION: DISEASE

FILE REFERENCE: 07891/009003

CURRENT APPLICATION NUMBER: US/09/617,053A

CURRENT PILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800,929

PRIOR ELING DATE: 1997-02-13

MIMMER OF SEG IN NOC: 17
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                           826 TATGAAGCACGGATCTTTACTTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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100.0%; Score 198; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.3e-59;
Matches 198; Conservative 0; Mismatches 0;
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OTHER INFORMATION: n can be any nucleotide
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
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ORGANISM: Homo sapiens
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US-09-617-053A-3
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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Eaird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: LAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
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                                                                        GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
Gaps
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; OTHER INFORMATION: N at 4622 and 4633 can be A, US-08-800-929A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
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APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08800929A Patent No. 6133437
                                                                                                                                                                                                          1006 CCAGGGTGCAAATATCTG 1023
                                                                                                                                                              181 CCAGGGTGCAAATATCTG 198
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US-08-511-485-9

US-08-511-485-9

Sequence 9, Application US/08511485

Sequence 9, Application US/08511485

Parent No. 5919912

APPLICANT: MacKenzie, Alexander E. APPLICANT: MacKenzie, Alexander E. APPLICANT: BAITG. Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, TITLE OF INVENTION: PROBES, AND DETECTION METHODS

NUMBER OF SEQUENCE ADDRESS: 3

CORRESPONDERCE ADDRESS: 3

COMPUTER: Doston

TITLE OF INVENTION: Street

CITY: Boston

COMPUTER: Law R. Compatible

COMPUTER: Law PC compatible

COMPUTER: Law PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/511,485

FILING DATE: A-10-1995

CLASSIFICATION ADDRESS: 07440(-1995

CLASSIFICATION WINDER: 30,162

MACTICAN PROPERATION NUMBER: 07540(002001

TELECOMMUNICATION INPORMATION:

REPRESENCE/DOCKET NUMBER: 07540(002001

TELECOMMUNICATION INPORMATION:

REPRESENCE/DOCKET NUMBER: 07540(002001

TELECOMMUNICATION INPORMATION:

REPRESENCE/DOCKET NUMBER: 07540(002001

TELECOMMUNICATION INPORMATION:

REPRESENCE 1001642-500

TELECOMMUNICATION INPORMATION:

TEL
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Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0

Qy 1 TATGAAGCACGGATCTTTACTTTTGGACATGGATATACTCATTAACAAGGAGCAGCTT 60

Db 916 TATGAAGCACGGATCGTTACTTTTGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 775

 121 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180

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Db 1096 CCAGGGTGCAAATACCT 1112
Search completed: October 22, 2004, 22:14:05
Job time: 55 secs

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GenCore version 5.1.6
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                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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198
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9b_htc:*:

9b_htc:*:

9b_est43:*:

9b_est6:*:

9b_gss1:*:
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716
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504
334
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                                       nucleic search,
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Perfect score:
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/note="Vector: pCMV-SPORT6"
                                                                                                                                                                 /organism="Homo sapiens"
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Best Local Similarity
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AUTHORS
TITLE
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Rlausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hasih, R.K.,
Esplechon, M., Soares, M.M., B., Bonaldo, M.F., Casavanch, T.L.,
Scheetz, T.E., Brownstein, M.J. Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Gargia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Retteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shewchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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Homo sapiens baculoviral IAP repeat-containing 8, mRNA (cDNA clone
                                                     121 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
                                                                                                      275 GGGGGGCTAACTGATTGGAAGCCCAGCGAAGACCTTGGGAACAACATGATAAATGGCAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1851)
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Submitted (25-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
215 TCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGAAAGTAAAGTGCTTTCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs.remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                            181 CCAGGGTGCAAATATCTG 198
                                                                                                                                                                                              335 CCAGGGTGTAAATATCTG 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BC056914
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TITLE
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SOURCE
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BC056914
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Clone distribution: MGC clone distribution information can be found through the I.M.AG.B. Consortiun/LinL at: http://image.llnl.gov Series: IRAK Plate: 119 Row: h Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: marched mRNA gi: 16974127
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD350778 173 bp mRNA linear EST 09-JUL-2003
UI-M-GIO-cgh-g-23-0-UI.rl NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:6853392 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Musinamalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Lo 773)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1062 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTACTCCGTTAACAAGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                                                                                               /mol type="mRNA"
/db_xref="taxon:9606"
/clone="ImAGE:574294"
/clone lib="NIH MGC 119"
/lab_bost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.8%; Score 166; DB 3;
ilarity 89.9%; Pred. No. 1.1e-40;
Conservative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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Matches 177; Conservative
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                                                                                       /ctoue="Organ Brain; Vector: pyx- Asc; Site 1: BCOR I; Site 2: Not 1; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcse gel. First strand CDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Pervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford CA 94305
Meb site:
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1789 bp mRNA linear HTC 13-FEB-2003 Howo sapiens, similar to baculoviral IAP repeat-containing 8, clone IMAGE:5742590, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGGCTAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTTCACTGTGGAGGAGGGCTCA 120
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (31-2MN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCAGTTGCAAGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 164.6; DB 6; Length 773; Pred. No. 2.2e-40;
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
|lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP GIO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
'tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                program coordinator."
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92.5%;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Plate: 107 Row: i Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein. This clone has the following problem: frame shifted. Incation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1002 TATGAAGCCCGGCTCATTATGGGACATGGATGTACTCCCGTCAACAAGAGAGCAGCTT 1061
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 628)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood, K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TATGAAGCACGGATCTTTACCTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Brain, adult medulla"
/clone lib="NIH MGC_119"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.0%; Score 164.4; DB 3;
89.4%; Pred. No. 3.4e-40;
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                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:5742590"
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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AI573382.1 GI:4536756
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145 AGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATATCTG 198
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/db_xref="taxon:9606"
/clone="NT2RM1000921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity
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Matches 114;
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                                                                                                           /tissue type="Teel"
/dev_stage="M30 CD4+ cells"
/dev_stage="M30 CD4+ cells"
/dev_stage="M30 CD4+ cells"
/deb_note="Solar (Kanamycin resistant)"
/clone lib="Stratagene mouse Tcell 937311"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
/note="Organ: blood; Vector: blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1177 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 TAIGAAGCACGGATCGTTACTTTTGGNACATGGACATCCTCAGTTACAAAGGAGCAGCTT 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 GGAGGCTCACGGATTGGAAGTCCAAGTGAAGACCCTTGGGAACAGCATGCGAAGTGGTAC 426
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
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/clone_lib="NIH MGC_124"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapDs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlade: LLAML2724 row: m column: 06
High quality sequence stop: 409.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 157.4; DB 1; Length 628;
Pred. No. 3.8e-38;
0; Mismatches 18; Indels 1
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/db_xref="taxon:9606"
/clone="IMAGE:5728685"
/tissue_type="hippocampus"
'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                            /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CCAGGGTGCAAATATCT 197
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Homo sapiens
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Les 178; Conserv
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TITLE
JOURNAL
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(destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is Oligo-dr primed and directionally cloned (Ecoxy site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotti, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 536)
Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K., Makamura,Y., Nagai,T., Sugano,S. and Isogai,T.
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K., Nakamura,Y., Nishikawa,T., Suzuki,Y., Kawai,Y., Ohpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                            85 GGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGATTGGAAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 AGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATATCTG
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Pred. No. 5.9e-24;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                   0; Indels
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1532-3 Yana Kisarazu, Chiba 292-0812, Japan
151: 81-438-52-3985
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                       Pred. No. 1.8e-24;
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                                                                                                                                                                                                                                                                                             100.0%; Pred. No.
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ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

ACCESSION VERSION

RESULT 8 AV706807 LOCUS

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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/irssources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 617)
Arakwa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Komo,H., Koya,S., Matsuyama,T., Ito,M., Kawai,J., Konno,H., Kowda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,Y., Shinagawa,A., Shiraki,T., Saogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashi,Zaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTTTTC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="spontaneous tumor, metastatic to mammary. Stem call origin."
/lab_host="DH10B"
/clone lib="NGI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo d'
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AGCAGCTTGCAAGAGTTGGATTTTAAGCTTTAGGTGAAGGCGATAAAGTCAAGTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB663325 RIKEN full-length enriched, 15 days embryo head Mus
musculus CDNA clone D930039G22 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 ACTGTGGAGGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 ACTGTGGAGGAGGCTCTCGGATTGGAAGCCAAGTGAAGACCCTTGGGAACAA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 100.2; DB 2;
Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: polyT not found Seg primer: -40UP from Gibco High quality sequence stop: 226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                     ity sequence stop: 226.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:3676174"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 92.9%;
Matches 105; Conservative (
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Best Local Similarity
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BB663325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                         AV706807 ADB Homo sapiens clone ADBCOF01 5', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z. Homo sapiens cDNA ADB clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. S. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 GCTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGGGGCTAACTGATTGGAAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATATCTG 198
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .<u>`</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Adrenal
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="ADB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="ADBCOF01"
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                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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CE100865 17000371110448 Dog Library Canis familiaris genomic,
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)
Arakawa,T., Carninoi,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 TTAGGGGATGGTGATAAAGTAAAATGCTTTCACTGTGGAGGAGGACTAACTGATTGGAAG 112
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 721)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9615"
/clone lib="hog Library"
/note="Site l: BetXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 4.9e-19;
0; Mismatches 6;

    .721
    /organism="Canis familiaris"

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/strain="Standard Poodle"
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Mus musculus
                                                                                                                                                                                          genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                 CE100865
CE100865.1 GI:35167750
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Canis familiaris
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Best Local Similarity 94.3%;
Matches 100; Conservative (
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228 CCT 230
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BB650856
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                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)
Konno, H., Fukumishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript XS(+) after bulk excision from Lambda FLC I"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inote="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 TTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="head"
/dev_stage="15 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="D930039G22"
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Best Local Similarity 87.89
Matches 108; Conservative
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REFERENCE AUTHORS

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207 GGNGAAGGCGATAAAGTGAAGTGCTTTCACTGGGGAGGAGGGCTCACGGATTGGAAGCCA

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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashi,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                               Email: genome-resaggsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-184-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="RIKEN full-length enriched, 0 day neonate cerebellum"
Takahashi, F.,
and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
., Tagawa, A.,
Muramatsu, M.
                                              RIKEN Mouse ESTB (Arakawa,T., et al. 2001)
Unpublished (2001)
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/dev_stage="0 day_neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .504
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  Sogabe, Y., Suzuki, H., Tagami, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/clone="C230036005"
                     Toya, T.,
                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                             Tanaka, T.,
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[Invitrogen:
sex="Male"
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Best Local Similarity 89.4
Matches 101; Conservative
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1 8 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/Chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/Chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. Coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed
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/dev_stage="12.5-dpc"
/lab_host="Maln0s"
/clone lib="MIA Mouse 12.5-dpc Male Genital
/clone lib="MIA Mouse 12.5-dpc Male Genital
Ridge/Mesonephros cDNA Library (Long)" is it = 1: Sall; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (Gonome Res.
11: 1553-1558 (Gonome Res.
DNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 314)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                      EST 07-JUN-2003
                                                                                                                                                                                                             C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros CDNA Library (Long) Mus musculus CDNA clone NIA:C0935E08 IMAGE:30037975 3', mRNA sequence.
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Laboratory of Genetics
Mational Institute on Aging/National Institutes of Health
Plateir Consell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: chaa@lgsun.grc.nia.nih.gov
Plate: C0935 row: E column: 08
Beg primer: -2nnl3 Forward
High quality sequence stop: 334
                                                                   319
145 AGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATATCT 197
                                          267 AGTGAAGACCCTTGGGAACAGCGAAGTGGTGCTACCCAGGGTGCAAATACCT
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db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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PUBMED
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KEYWORDS
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CF222542
AGENCOURT_14926978 NICHD_XGC_EMb5 Xenopus tropicalis cDNA clone
IMAGES 6981334 5', mRNA sequence.
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/dev_stage="embryo, stages 10-13"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
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cloned undirectionally. Primer: Oligo dT. Average insert
size 2.0 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGGGCTAACTGGATGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Ronpodinae; Xenopus; Silurana.

( Chases 1 to 791)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Carder Institute / NIH
Bldg. 31 Rm 0A07 Bethesda, MD 20892
Bmall: Ggapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                  200 CCAAGTGAAGACCCTTGGGAACAGCATGCGAAGTGGTACCCAGGGT 155
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                                    142 CCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGT 187
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Pred. No. 2.9e-17;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)

    .791
    /organism="Xenopus tropicalis"

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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 3
High quality sequence stop: 735.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                          CF222542.1 GI:33423250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGGTGCAAATATCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.9%;
Best Local Similarity 66.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ552032 584 bp mRNA linear BST 20-JUN-2002 H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone H4013A06 3', mRNA sequence.
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Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
Smail: Casell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Seg primer: -21M13 Forwar A column: 06
Seg primer: -21M13 Forwar High quality sequence stop: 584
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                                                                                                                                                                    82 TIAGGIGAAGGIGAIAAAGIAAAAGIGCITICACIGIGGAGGAGGAGGCIAACIGAIIGGAAG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="mixed"
/lab_host="DH10B"
/clone lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Vector: pSPORTH; Site 1: Sall; Site 2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Assembly, verification, and initial annotation of NIA 7.4K mouse Genome Res. 12 (12), 1999-2003 (2002)
                                                                                                                                Gaps
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0
                                                                               Length 334;
                                                                                                                                                                                                                                                                   142 CCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGT 187
                                                                                                                                                                                                                                                                                                  200 CCAAGTGAAGACCCTTGGGAACAGCATGCGAAGTGGTACCCAGGGT 155
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                                                                        Score 91.6; DB 4;
Pred. No. 1.2e-17;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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46.3%; Score 91.6; DB 5;
Best Local Similarity 91.5%; Pred. No. 1.5e-17;
Matches 97; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="niaEST:H4013A06-3"
/db_xref="taxon:10090"
/clone="H4013A06"

    584
    forganism="Mus musculus"
/mol_type="mRNA"
    fstrain="C57BL/6"

by Yulan Piao (NIA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                      0;
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                                                                     ch 46.3%;
1 Similarity 91.5%;
97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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Best Local S
Matches 97
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MEDLINE PUBMED

COMMENT

FEATURES

JOURNAL

TITLE

ACCESSION

VERSION KEYWORDS

REFERENCE AUTHORS

RESULT 14

447 ccrccarccaagrrccrc 464

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260 TTAGGTGAAGGCGATAAAGTGAGTGCTTTCACTGTGGAGGAGGCTCACGGATTGGAAG 201

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ORIGIN

Search completed: October 22, 2004, 22:12:14 Job time: 1732.5 secs

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61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                            Length 2100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 224, Application US/10636065
; Sequence 224, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
   APPLICANT: Rorneluk, Robert G.
   APPLICANT: LaCase, Eric
   APPLICANT: Baird, Stephen
   APPLICANT: Holcik, Martin
   APPLICANT: Woung, Sean
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: Thereof
   TITLE OF INVENTION: QUARANTE OF SEAD
   TITLE OF INVENTION: Thereof
   FILE REFERENCE: 07891/02505
   CURRENT FILING DATE: 2003-08-07
   PRIOR APPLICATION NUMBER: 09/672,717
   PRIOR APPLICATION NUMBER: 09/672,717
   RIOR APPLICATION NUMBER: 09/672,717
   RIOR APPLICATION NUMBER: 2000-09-28
   NUMBER OF SEQ ID NOS: 231
   SOFTWARE: FESTERE FOR Windows Version 4.0
   SEQ ID NO 224
   LENGTH: 2100
                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                              87.4%; Score 173; DB 9;
92.4%; Pred. No. 2.9e-46;
tive 0; Mismatches 15;
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER PLICATION NUMBER: 08/511,485
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.4
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9
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Best Local
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87.4%; Score 173; DB 17; Length 2100;

Best Local Similarity 92.4%; Pred. No. 2.9e-46;

Matches 182; Conservative 0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMALLIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMALLIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE REPRENCE: 07891/003006.272
CURRENT APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-08-04
1036 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGAACAGA
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                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/10600272; Publication No. US20040157232A1; GENERAL INFORMATION:
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                                                                                                                            181 CCAGGGTGCAAATATCT 197
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CORGANISM: Mus musculus
US-10-600-272-9
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Sequence 3, Application US/09974592

Batent No. US20020120121A1

GENERAL INFORMATION:
APPLICANT: MacKenzie, Alexander B
APPLICANT: Baird, Beter
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Pang, Benjami
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100.0%; Score 198; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-54;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTATION: 4623
COTHER INFORMATION: n can be any nucleotide NAME/KEY: variation variation 4622
COTHER INFORMATION: n can be any nucleotide US-09-974-592-3
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ORGANISM: Homo sapiens
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LENGTH: 5232
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                                                                                                                                                                                                                                                                                             61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGAGGCCTAACTGGTAGGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 180
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                                                                                                                                                                                                                                                       1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                           100.0%; Score 198; DB 17; Length 2540; 1100.0%; Pred. No. 1.9e-54; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 231, Application US/10636065

Publication No. US20040127694A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: LaCasse, Eric

APPLICANT: Baird, Stephen

APPLICANT: Young, Sean

TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

TITLE OF INVENTION: Thereof

FILE REFERENCE: 07931/025005

CURRENT APPLICATION NUMBER: US/10/636,065

CURRENT APPLICATION NUMBER: 09/672,717

PRIOR APPLICATION NUMBER: 09/672,717

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 231

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 231

LENGTH: 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 198; DB 17; Length 100.0%; Pred. No. 2e-54; tive 0; Mismatches 0; Indels
                 ) LOCATION: (2540)

) OTHER INFORMATION: N may be any nucleotide

US-10-600-272-3
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                                                                                                                                                                                             Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo sapiens
US-10-636-065-231
NAME/KEY: variation LOCATION: (2540)...
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-636-065-231
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Sequence 9, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: MacKenzie, Alexander E.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
ITILE OF INVENTION: PROBES, AND DETECTION METHODS
ITILE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT APPLICATION: UNDRES: US/09/201,936
CURRENT FILING DATE: 1998-12-01
ERALIER APPLICATION NUMBER: 09/011,356
BARLIER FILING DATE: 1998-02-04

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Sequence 3, Application US/10600272 Publication No. US20040157232A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCAGGGTGCAAATATCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                | LOCATION: (1) ... (2540)
| OTHER INFORMATION: n=a,t,c, or g
US-10-636-065-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
      LaCasse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
      APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGAGGGCTAACTGGTTTGGAAGCCCCAGTGAAGACCTTGGGAACAACAACAAGTGGTAT 180
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                                                                                                                     THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 198; DB 16; Length 2540; 100.0%; Pred. No. 1.9e-54; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURREAL AFFLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION LUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
FILING DATE: CHNKNOWN>
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0001 US
REGISTRATION NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 91184319
SEQUENCE DESCRIPTION: SEQ ID NO: 900
                                                                                 Susan G. Stuart
Susan G. Stuart
Jeffrey 7. Seilhamer
Jeffrey 7. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccadedrecaaararcre 1023
Sequence 900, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Bentain G.
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                     NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                         CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: GENBANK
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Best Local Similarity 100.
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304
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Sequence 218, Application US/10636065 Publication No. US20040127694A1 GENERAL INFORMATION:

US-10-636-065-218

RESULT 9

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APPLICANT: MacKenzie, Alexander B.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/06306
CURRENT PELLING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/10/600,272
CURRENT FILING DATE: 1998-02-04
PRIOR PILING DATE: 1998-02-04
PRIOR PILING DATE: 1996-08-05
PRIOR PILING DATE: 1996-08-05
PRIOR PLICATION NUMBER: US 08/576,956
PRIOR PLICATION NUMBER: US 08/576,956
PRIOR PLICATION NUMBER: US 08/511,485
PRIOR PLICATION NUMBER: US 08/511,485
PRIOR PLICATION NUMBER: US 08/511,485
APPLICANT: Baird, Stephen
APPLICANT: Baird, Martin
APPLICANT: Baird, Martin
APPLICANT: Woung, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: 08/10/636,065
CURRENT APPLICATION NUMBER: 09/672,717
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR PELING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 218
LENGTH: 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 198; DB 17; 100.0%; Pred. No. 1.9e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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SCHWARLE INFORMATION NUMBER: US 60/412,049

PRICANT: GENOMIC HEALTH

APPLICANT: BAKET, JOÉTE B.

APPLICANT: Cronin, Maureen T.

APPLICANT: Kréfer, Michael C.

APPLICANT: Kréfer, Michael C.

APPLICANT: Shak, Steve

APPLICANT: Malker, Michael Graham

TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES

CURRENT APPLICATION NUMBER: US/10/388,360

CURRENT FILING DATE: 2003-03-12

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 384

SEQ ID NO 331

LENGTH: 2540
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                                                                                                                                                                                                                                       61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
                                                                                                                                                                                                                                                                 121 GGAGGGTAACTGATTGGAAGCCCAGTGAAGACCGTTGGGAACAACATGCTAAATGGTAT
                                                                                                                                                      1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                       Length 2540;
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                                                                                                                            Indels
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                                                                   Query Match
100.0%; Score 198; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. Mo.
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Publication No. US20030225528A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CCAGGGTGCAAATATCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1006 CCAGGGTGCAAATATCTG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-388-360-331
                            US-10-366-307-1
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                                                                                                                 Sequence 274, Application US/10007926A

Sequence 274, Application US/10007926A

Sequence 274, Application No. US20030143539A1

SEGUENCE INPORMATION:

APPLICANT: BERTUCCI, FRANCOIS

APPLICANT: HOULGATTE, RENT

APPLICANT: HOULGATTE, RENT

APPLICANT: PIRNBAUM, DANIEL

APPLICANT: VIENS, PATRICE

APPLICANT: VINCENT

TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

CURRENT APPLICATION NUMBER: US/10/007,926A

PRIOR APPLICATION NUMBER: 60/254,090

NUMBER OF SEQ ID NOS: 468

SOFTWARE PATENTING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 468

SOFTWARE PATENTING DATE: 2000-12-08

SOFTWARE PATENTING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 945
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TITLE OF INVENTION: Methods for Determining the Prognosis
TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
TITLE OF INVENTION: for Patients with a Prostate Neoplastic CORRENT PLUS 5659
CURRENT PILING DATE: 2003-02-12
PRIOR PAPLICATION NUMBER: US 0/356,956
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
IENGTH: 2540
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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100.0%; Score 198; DB 15; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4)
OTHER INFORMATION: gene.
1006 CCAGGGTGCAAATATCTG 1023
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Publication No. US20030224399A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                    US-10-007-926A-274
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US-10-641-643-900

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100.0%; Score 198; DB 9; Length 2540;
Best Local Similarity 100.0%; Pred, No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0
                                              ..
Length 2404;
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GENERAL ILLOGRATION;
APPLICANT: Kornelluk, Robert G.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN DETECTION METHODS
TITLE OF INVENTION: MAMBER: US/09/201,936
CURRENT PILLING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: POT/1B96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER PILLING DATE: 1996-08-05
EARLIER PILLING DATE: 1995-08-05
EARLIER FILLING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 3
LENGTH: 2540
LENGTH: 2540
                                              Indels
    100.0%; Score 198; DB 9;
100.0%; Pred. No. 1.8e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (2540) ... (2540) OTHER INFORMATION: N may be any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09201936; Publication No. US20020187946A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              1007 CCAGGGTGCAAATATCTG 1024
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                Query Match
Best Local Similarity 100.0
Matches 198; Conservative
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Publication No. US20040c10136A1

Publication No. US20040c10136A1

GENERAL INFORMATION: Janice K.; Seilhamer, Jeffrey J.

APPLICANT: AT-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON

CURRENT APPLICATION NUMBER: US/10/305,720

CURRENT APPLICATION NUMBER: 09/016,434

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 1490

SOFTWARE: PERL PROGRAM

SEQ ID NO 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                994 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1053
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Sequence 38, Application US/09964899

Sequence 38, Application US/09964899

Patent No. US20020174446A1

GENERAL INFORMATION:
APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-11612 A

CURRENT PELICATION NUMBER: US/09/964,899

PRIOR FILING DATE: 2001-09-27

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LEATH: 2404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      874 TAIGAAGCACGGATCITTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | NAME/KEY: misc feature
| CTHER INFORMATION: GenBank ID No. US20040010136A1 g1016687
| US-10-305-720-1053
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                                                                                                   1006 CCAGGGTGCAAATATCTG 1023
                                                            181 CCAGGGTGCAAATATCTG
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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US-10-305-720-1053
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US-09-964-899-38
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Published Applications NA:\*

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9: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
10: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
11: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
13: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
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17: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
18: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
19: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
19: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
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21: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
22: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
22: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
22: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\*
22: /cgn2\_6/ptodata/2/pubpna/US108\_PUBCOMB.seq:\* 22: 33: 44: 46: 110: 114: 114: 118: 210: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 1053, Ap Sequence 38, Appli Sequence 274, App Sequence 174, App Sequence 311, Appli Sequence 311, App Sequence 218, App Sequence 218, App Sequence 21, Appli Sequence 21, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Description SUMMARIES П Query Match Length DB 1588 1659 2404 2540 2540 2540 2540 2540 2540 3000 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Score 198 198 198 198 198 198 198 198 110 110 111 12 Result No.

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6-9	US-09-974-592	US-10-343-115	US-10-343-11	US-IU-UZ4-433-I	135	T=/04-669 ST SS	TIS-10-103-601	IIS-10-305-324-	US-10-641-643-80	IIS-10-232-286-2	3-201-036-	3-10-636-06	, , ,	נ	- C	15-/75-	00-904-456	-02-334-331-I	T .	ζ,	116-827-	2T9-T4T	5	1/2-118-	-10-3	-10-	US-10-353-461-7		-671-1	974-592-5	
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87.4 87.4 87.4	· LO ·	83.8	7			48.9	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	. 6			•	39.7	0		١σ	•		ή,	o,		39.7	
173 173 173	169.8	166	164.4	157.8	131.4	96.8	78.6	78.6	78.6	œ.	78.6		78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6		0.0	0 0	78.6	78.6	78.6	
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# ALIGNMENTS

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SULT 1 -10-024-433-3 Sequence 3, Application US/10024433 Sequence 3, Application US/10024433 Sequence 4, Application No. US2020086409A1 Dubblication No. US20020086409A1 GENERAL INFORMATION: APPLICANT: Robert G. Korneluk et al. TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING FILE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING FILE REFERENCE: 07891/01802 CURRENT APPLICATION NUMBER: US/10/024,433 PRIOR APPLICATION NUMBER: 09/239,867 PRIOR FILING DATE: 1999-01-29 PRIOR FILING DATE: 1999-01-29 SOFFWARE: FastSEQ for Windows Version 4.0 LENGTH: 1588 TYPE: DAA ORGANISM: Homo sapiens 10-024-433-3	100.0%; Score 198; DB 13; Length 1588; 100.0%; Pred. No. 1.5e-54; vative 0; Mismatches 0; Indels 0; Gaps CGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 60 CGGATCTTTACTTTTGGGACATGGATAATACTCAGTTAACAAGGAGCAGCTT 88 SGATCTTTAGCTTTAGGTGAAGTGATAAGTAAAGTAACAAGGAGCAGCTT 88 SGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 12
SULT 1 -10-024-433-3 Sequence 3, Application 1 Publication No. US202006 GENERAL INFORMATION: APPLICANT: Robert G. Kor TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION: METH TITLE OF INVENTION WINGER FILE REFERENCE: 07891/01 CURRENT FILING DATE: 1999- PRIOR FILING DATE: 1999- PRIOR FILING DATE: 1999- NUMBER OF SEQ ID NOS: 10 SOFTWARE: FASTSEQ FOR WINGER TURN: 1588 TYPE: DATE ORGANISM: HOMO SADIENS TYPE: DATE ORGANISM: HOMO SADIENS	O) W
RESULT 1 US-10-024-433-3 Sequence 3, Ag Publication N GENERAL INFORM TITLE OF INVE TITLE OF INVE TITLE OF INVE CURRENT APPLICANT: CURRENT APPLICANT: CURRENT PILING NUMBER OF SEQ SOFTWARE: FAS SEQ ID NO 3 LENGTH: 1588 SEQ ID NO 3 LENGTH: 1588 TYPE: DNA TYPE: DNA CUS-10-024-433-3	Query Match Best Local Matches 19 Oy 1 Db 826 Oy 61 Ob 886

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GenCore version 5.1.6
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Scoring table: IDENTITY NUC Gapext 1.0

	residues
Gapop 10.0 , Gapext 1.0	4526729 seqs, 23644849745 residues
	Searched:

eters: 9053458		
Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%

45 summaries	
Listing first	GenBmbl:* 1: gb ba:* 2: gb htg:* 3: gb_in:* 4: gb_om:* 5: gb_ow:* 6: gb_pat:* 7: gb_ph:* 8: gb_pt:* 10: gb_re:* 11: gb_re:* 12: gb_w:* 13: gb_w:* 14: gb_v:*
	Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	00000000000000000000000000000000000000	AR435474 Semience	AR451574 Semience	AR473584 Semience	AX412124 Semience		AP116702 Compane		AD370620 SOCIOUS	AVERGE SEGMENTS	TIBBOOD MAR THERE	TISEBLA MAR MARCALL	ACTATION WINDOWS	ACT09227 Mis miscu	AF184429 Dattie no	AR033366 Pattic no	DF304334 Dattus no	AF304333 Dattie no	AR263641 Sequence
SUMMARIES		ID	AR302739	AR435474	AR451574	AR473584	AX412124	AR106400	AR116702	BD190871	AR370620	AX670906	MMIB8990	) MMU36842	0 AC137152	AC109227	) AF183429	3 AB033366	) AF304334	) AF304333	AR263641
		Match Length DB	2100 6	2100 6	2100 6	2100 6	2100 6	2691 6	2691 6	2691 6	2691 6	2691 6	2691 1	1988	179719 1	205211 2	1491	2468 1	3032 1	2032 1	1588 6
9/0	Query	Match ]	100.0	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	98.4	98.4	94.3	93.5	93.5	91.9	91.9	91.9	91.1	87.4
		Score	198	198	198	198	198	194.8	194.8	194.8	194.8	194.8	194.8	186.8	185.2	185.2	182	182	182	180.4	173
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RESULT 2

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87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	79.3	79.3	79.3	
173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	173	157	157	157	
20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	. 39	40	41	42	43	44	45	

# ALIGNMENTS

RESULT 1

Title: US-09-654-743-51
Perfect score: 198
Sequence: 1 tatgaagcacggatcgttac.....acccagggtgcaaataccta 198

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976 gcaagagcrogarfriardcrifraggroaaggcgaraaagroaagroaagrocrocrororoga 1035
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                 1036 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1095
                                                                                                                                                                               PAT 20-FEB-2004
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2100)

Korneluk, R.G., MacKenzie, A.E., Baird, S. and Liston, P.
Mammalian IAP gene family, primers, probes and detection methods
Patent: US 6689562-A 9 10-FBB-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Patent: WO 0226958-A 224 04-APR-2002;
University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
Location/Qualifiers
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100.0%; Pred. No. 1.5e-45;
iive 0; Mismatches 0;
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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SAX412124 AX412124.1 GI:21444584
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Sequence 9 from patent US 6689562.
                                                                                                                                                                                                                                                                                                                                                                                                  1. .2100
/organism="unknown"
/mol_type="genomic DNA"
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                                                                                       1096 CCAGGGTGCAAATACCTA 1113
                                                                    CCAGGGTGCAAATACCTA 198
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                                                                                                                                                                                                                                                                                    Unknown.
Unclassified.
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AR473584.1
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Unknown.
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AX412124
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                        PAT 18-DEC-2003
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                                                                                                                                                       1 (bases 1 to 2100)

Korneluk, R.G., MacKenzie, A.E., Baird, S. and Liston, P.
Mammalian apoptosis inhibitor protein gene family, primers, probes and detection methods
Patent: US 6656704-A 9 02-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                      975
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Unclassified.
1 (bases 1 to 2100)
Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
Antisense IAP uncleic acids and uses thereof
Patent: US 6673917-A 224 06-JAN-2004;
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Pred. No. 1.5e-45;
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Sequence 224 from patent US 6673917.
AR451574
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                 2100 bp
Sequence 9 from patent US 6656704.
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                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 100.
Matches 198; Conservative
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                                                                                                                                         Unclassified.
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Best Local Similarity
Matches 198; Conserv
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          AR435474
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BD190871 2691 bp DNA linear PAT 17-JUL-2003 Detection and modulation of the IAPs and NAIP for the diagnosis and treatment of proliferative disease.
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Patent: JP 2002512602-A 4 23-APR-2002;
UNIVERSITY OF OTTAWA.
                                                                                                                                                                                                                                                                                                                                                                   61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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G01N33/574,
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23-APR-2002
13-FEB-1999 JP 1998531325
13-FEB-1997 US 08/800329
ROBERT KORNELUK, ALEXANDER E MACKENZIE, PETER LISTON, STEPHEN
       Unclassified.
1 (bases 1 to 2691)
Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K.
                                                                                                                                                                                                                                                                                                                                 1461 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT
                                                        Pratt,C.
Modulation of IAPs for the treatment of proliferative diseases
Patent: US 6133437-A 9 17-0CT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequences.
1 (bases 1 to 2691)
Korneluk,R., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B. and
                                                                                                                                                                                                                                                                                                 1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                                        Score 194.8; DB 6;
Pred. No. 1.1e-44;
0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                 1. .2691
/organism="unknown"
/mol_type="unassigned DNA"
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Strandedness: Single;
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Best Local Similarity 99.0%;
Matches 196; Conservative
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Best Local Similarity
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Patent: US 6107041-A 9 22-AUG-2000;
Location/Qualifiers
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Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and
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                                                                                        916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                       1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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   Length 2100;
                                       Indels
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Query Match 100.0%; Score 198; DB 6; )
Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 198; Conservative 0; Mismatches 0;
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Sequence 9 from patent US 6107041.
AR106400 GI:12820930
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Sequence 9 from patent US 6133437.
AR116702
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Best Local Similarity 99.0<sup>5</sup>
Matches 196; Conservative
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SOURCE ORGANISM

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DEFINITION

RESULT 6 AR106400 LOCUS

ACCESSION VERSION KEYWORDS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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RESULT 7 AR116702 LOCUS

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MMUB8990 2691 bp mRNA linear ROD 31-MAY-1997
Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA,
complete cds.
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                                                     Pratt, C. Modulation of the laps and naip for the treatment of proliferative
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Mustaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 2691)

1 (bases 1 to 2691)

Rardanni, K., Lefebvre, C., Korneluk, R.G. and MacKenzie, A.B.

Genomic Organization and Primary Characterization of miap-3: The

Murine Homologue of Human X-linked IAP
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2 (bases 1 to 2691)

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                        Korneluk, R., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.
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Pred. No. 1.1e-44;
0; Mismatches 2; Indels 0;
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                                                                                                                           Patent: EP 1277836-A 9 22-JAN-2003;
University of Ottawa (CA)
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/dev stage="embryo"
1. .2691
/gene="miap-3"
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/gene="miap-3"
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1 (bases 1 to 2691)
Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and
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Wus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                     1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Sequence 9 from Patent BP1277836.
AX670906
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Sequence 9 from patent US 6300492.
AR370620 GI:34607376
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Uren, A.G., Pakusch, M., Hawkins, C.J., Puls, K.L. and Vaux, D.L.
Cloning and expression of apoptosis inhibitory protein homologs
that function to inhibit apoptosis and/or bind tumor necrosis
factor receptor-associated factors
Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
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99.0%; Pred. No. 1.1e-44;
ative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus IAP homolog A (MIHA) mRNA, complete cds.
      'product="X-linked inhibitor of apoptosis"
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2 (bases 1 to 1988)
Vaux, D.L., Uren, A.G. and Pakusch, M.
Direct Submission
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                                                                                                                                                                                                                                                 1646. .1724
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                                                                                                                                                                                                    1546. .1645
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gene="miap-3"
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                                                                                                                                                                                                                                                                                                725. .1767
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ICMDRNIATUFPVGGGLTVTKQCAEAVDKCPMCXTVITFRQKIFNS:
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Mus musculus chromosome UNK clone RP24-269A16, complete sequence.
AC137152
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        The Walter and Eliza Hall Victoria 3050, Australia
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Submitted (21-SEP-1995) M. Pakusch,
Institute, Royal Parade, Parkville,
                                                                                                                                                             6 x CBA"
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1. .1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="BIR repeat 3"
1556. .1660
/gene="MIHA"
/note="RING finger"
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                             Institute, Royal Parade, Pari
Location/Qualifiers
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001. .1198
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product="MIHA"
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/gene="MIHA"
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Best Local Similarity 96.5%;
Matches 191; Conservative
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(bases 1 to 205211)
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                                                                                                                                               McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (18-NOV2002) Genome Sequencing Center, 4444 Forest Park
Tarkway, St. Louis, MO 63108, USA
3 (Dasses 1 to 179719)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-DEC-2003) Genome Sequencing Center, 4444 Forest Park
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                                                                                                                                                                                                                                                                                Submitted (27-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 179719)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC109227

Mus musculus chromosome 7 clone RP23-396C19 map 7, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
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HTG; HTGS PHASE2; HTGS FULLTOP, HTGS_ACTIVEFIN.
HTG: MUSS musculus (house moüse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 179719)

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                                                                                                                                                                                                                                                                                                                                                                                                        Parkway, St. Louis, MO 63108, USA On Dec 24, 2003 this sequence version replaced gi:25054276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.5%; Score 185.2; DB 10; Length 179719; 96.0%; Pred. No. 3e-42;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: M_BB0269A16
                                                                                          The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-269A16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holcik,M., Lefebvre,C.A., Hicks,K. and Korneluk,R.G.
Cloning and characterization of the rat homologues of the Inhibitor
of Apoptosis protein 1, 2, and 3 genes
BMC Genomics 3 (1), 5 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.
Direct Submission
Submitted (108-28P-1999) Department of Biochemistry, Microbiology and Immunology, University of Ottawa, 451 Smyth Road, Ottawa, Ontario KIH 8M5, Canada
Location/Qualifiers
1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                 Score 185.2; DB 2; Length 205211;
Pred. No. 2.9e-42;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="RIAP-3; similar to X-linked IAP (XIAP)"
                                                                                                                                                                                                                      /clone="RP23-396C19"
/clone_lib="RPCI-23 Female Mouse BAC"

    1491
    organism="Rattus norvegicus"

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Rattus norvegicus
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96.0%;
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Pred. No. 5.4e-41;
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Local Similarity 94.9%;
es 188; Conservative
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- nucleic search, using sw model nucleic

October 22, 2004, 19:31:13 Run on:

; Search time 261 Seconds (without alignments) 3982.319 Million cell updates/sec

US-09-654-743-51 Title: Perfect score:

1 tatgaagcacggatcgttac.......acccagggtgcaaataccta 198 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

8269772 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesegn2003cs:\* genesegn2003ds:\* N\_Geneseq\_23Sep04:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2004s:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* 55::7 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Apt 70839 Mondo		Miring					Himan		Aak99405 IND OF PD	Human a	Aaa64901 Human Y-1			X-linke		Adhalono BING-SH				
SUMMARIES	8 ID	2 AAT70839	5 ABK93872	2 AAV55041	8 ABZ58102	2 AAT72710	5 ABS52803	3 AAZ48862	10 ACA56455	12 ADI56251	5 AAK99405	2 AAT70836	3 AAA64901	5 ABK93869	5 ABV94283	3 AAL53731	3 AAD49663	9 ADB81002	L0 ADG89383	tl ADI31574	L2 ADH74638	12 ADL70165
	Query Match Length DB	2100	2100	2691	2691	1988	1588 (	1659	1659	1659	2404	2540	2540	2540	2540	2540 8	2540 8	2540	2540	2540	2540	2540
do	Query	100.0	100.0	98.4	98.4	94.3	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4
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87.4	87.4	79.3	75.3	75.3	75.3	74.4	74.4	74.4	73.6	72.8	67.9	55.4	40.3	39.3	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4
173	173	157	149	149	149	147.4	147.4	147.4	145.8	144.2	134.4	109.6	79.8	77.8	92	92	16	92	26	16	92	16	16
22	23	24	25	26	27	28	29	30	31	32	G 33	34	35	c 36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Mouse apoptosis inhibitor m-xiap cDNA. BP. AAT70839 standard; cDNA; 2100 (first entry) 02-SEP-1997 RESULT 1 AAT70839

Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis; ds.

Location/Qualifiers 127. .1617 /\*tag= a вb. Mus Key

WO9706255-A2 20-FEB-1997 

96WO-IB001022. 95US-00511485. 95US-00576956. 05-AUG-1996; 04-AUG-1995; 22-DEC-1995;

(UYOT-) UNIV OTTAWA.

Р, Liston Baird S, Mackenzie AE, Korneluk RG,

WPI; 1997-154262/14. P-PSDB; AAW19584.

of of Nucleic acid encoding an inhibitor of apoptosis polypeptide - used inhibit apoptosis in e.g. HIV or AIDS patients, and for detection or susceptibility to apoptotic disease.

Claim 11; Page 78-79; 219pp; English.

Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2

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genes (AAT70836-41) respectively code for a new class of mammalian proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The murine xiap gene (for X-linked IAP gene) sequence was constructed from 12 overlapping clones isolated from a mouse embryo lambda-gtil obwa library and from a mouse embryo lambda-gtil obwa library and from a mouse PIX II genomic library using human xiap cDNA as probentap nuclea caides can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                        121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                         975
                                                                                                                                                                                                                                                                                                                                         GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative
                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
                                                                                                                                                                                                                                                                                                       916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                        1 TATGAAGCACGGATCGTTACTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                     and disorders involving apoptosis (anti-apoptotic gene therapy)
                                                                                                                                                                                                      Length 2100;
                                                                                                                                                                       Seguence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xonug S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse cDNA encoding inhibitor of apoptosis, XIAP.
                                                                                                                                                                                                      Score 198; DB 2;
Pred. No. 2.4e-58;
                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCAGGGTGCAAATACCTA 198
                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK93872 standard; cDNA; 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001; 2001WO-CA001379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000; 2000US-00672717
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                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-479562/51.
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                                                                                                                                                                                                                        Local Similarity
les 198; Conserv
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                                                                                                                                                                                                            Query Match
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Matches
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ABK93872
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Disclosure; Fig 4; 135pp; English

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                                                                                                                                                                                                        sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a mouse IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                               of
         The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPI or HIAPI. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliozate, improve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 198; DB 6; 100.0%; Pred. No. 2.4e-58;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "XIAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine XIAP coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                         cDNA sequence
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                                                                                                                                    This sequence encodes the mouse XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with brolliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of everty, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor proteins are posisfance to chemotherapannic, arenes and minesting in the constant of the increase them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibitor of apoptosis, MIAP3; mouse; apoptosis; cancer; leukaemia; lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                          TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCCAGTTAACAAGGAGCAGCTT
       Pratt C;
                                                              Inducing apoptosis in proliferative mammalian cells with inhibitor or NAIP polypeptide - also methods for prognosis based on presence and NAIP, specifically applied to cancers involving p53 mutations.
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0
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                                                                                                                                                                                                                                                                                                                                               Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 U; 0 Other;
       Tsang B,
                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
      Baird S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse inhibitor of apoptosis protein MIAP3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
     Liston P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "MIAP3"
                                                                                                               Claim 13; Fig 4; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1641 ccadecrecaaraccra 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGTGCAAATACCTA 198
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                                                                                                                                                                                                                                                                                                                                                                         98.4%;
99.0%;
   Mackenzie AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672. .2162
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                         WPI; 1998-467164/40.
P-PSDB; AAW69297.
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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 Korneluk R,
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ABZ58102
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                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of cDNA encoding murine inhibitor of apoptosis protein MIAP3. The invention provides a nucleic acid, such as an antisense oligonucleotide, which specifically hybridises to a nucleic acid encoding an inhibitor of apoptosis protein, especially MIAP1, MIAP2, MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's conditions contacting the cell with the nucleic acid under use of a vector, liposome, or a mechanical or electrical means. The use of a vector, liposome, or a mechanical or electrical means. The nethod is used to treat acute lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 TATGAAGCACGGATCGTTACTTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA; degenerative disease; infectious disease; autoimmune disease; cancer; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.4%; Score 194.8; DB 8 99.0%; Pred. No. 3.5e-57;
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                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK.
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03-JUL-2002; 2002WO-US021002
                                             03-JUL-2001; 2001US-00898158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT72710 standard; DNA; 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 196; Conservative
                                                                                                                                           Shelanski
                                                                                                                                                                                         2003-210351/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                  P-PSDB; ABP72157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1997
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                                                                                                                                        Iroy CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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WO9723501-A1

03-JUL-1997

20-DEC-1996; 22-DEC-1995; WPI; 1997-350966/32. P-PSDB; AAW19745.

Vaux DL;

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GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of apoptosis) family of proteins that is expressed in the testes. (I) is useful for identifying a compound that modulates TIAP biological activity (I) is useful for increasing apoptosis in a cell, preferably a germ-line cell and for increasing fertility in an animal. (I) is useful for treating or preventing apoptosis which occurs as a part of testicular cancer and male infertility. TIAP may be manipulated for use as a male bith control. ITAP polypeptides and nucleic acid sequences also have diagnostic use in the detection or monitoring of conditions involving aberrant levels of apoptosis. The present sequence represents the coding sequence of X-linked inhibitor of apoptosis (XIAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                   /*tag= a
/transl except= (pos:34. .36, aa:Xaa)
/product= "X-linked inhibitor of apoptosis protein, XIAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide, a member of inhibitor of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells, particular cells involved in male fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGGAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAIGAAGCACGGAICGITACTITIGGAACAIGGAIATACAGTTAACAAGGAGCAGCII
                                                                                                           'note= "Start codon illegible in specification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 173; DB 6; Length 1588;
Pred. No. 1.2e-49;
0; Mismatches 15; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1588 BP; 505 A; 274 C; 359 G; 444 T; 0 U; 6 Other;
                                                                                                                                         represented as nnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ48862 standard; cDNA; 1659 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 4A; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1006 ccasssiscaararcr 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                18-DEC-2001; 2001US-00024433.
                                                                                                                                                                                                                                                                                                                            98US-0073001P.
99US-00239867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.4%;
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.1527
                                                                                             partial/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lagace M;
                                                                                                                                                                                                                                                                                                                                                                                                   (KORN/) KORNELUK R G.
(LAGA/) LAGACE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-642245/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABG32418.
                                                                                                                                                                                        US2002086409-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korneluk RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000
                                                                                                                                                                                                                                                                                                                              29-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                       29-JAN-1999;
                                                                                                                                                                                                                                      04-JUL-2002
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1001 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP homologue A (MIHA) (AAM19745), a murine homologue of baculovirus inhibitor of apoptosis protein (IAP). It was isolated from a mouse liver CDNA library on the basis of homology to Orgyia pseudotsuguta polyhedrosis virus IAP BIR and RING finger amino acid motifs. Animal IAP homologue nucleic acids (see also AAT72711-17) can be used to produce polyhedricals useful in methods for modulating apoptosis in animal cells, specifically for treatment, by inhibition, of degenerative and infectious disease or, by promotion, of cancer and autoimmune disease, and can be used for gene therapy of these diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                           Isolated protein homologues of viral inhibitors of apoptosis - used to modulate apoptosis for treatment of degenerative, infectious or auto:immune diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1061 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTTCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitor of apoptosis protein; IAP; testis; XIAP; apoptosis; TIAP; fertility; testicular cancer; male infertility; male birth control; X-linked inhibitor of apoptosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding X-linked inhibitor of apoptosis, XIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.3%; Score 186.8; DB 2;
96.5%; Pred. No. 1.9e-54;
tive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 44-47; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGGGTGCAAATACCTA 1198
                                                                                                                                                                                                                     (AMRA-) AMRAD OPERATIONS PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABS52803 standard; DNA; 1588 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGGTGCAAATACCTA 198
                                                                                                                             96WO-AU000827
                                                                                                                                                                           95AU-00007275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 96.5
Matches 191; Conservative
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Gaps

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885 120 945

15-NOV-2002

Mammalia

Key

ABS52803,

ABS52803

1181 181

61

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qq

Dp

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121

à

qq ð 엄 Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens

Human signalling pathway polynucleotide probe SEQ ID NO 1053

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This sequence encodes the human XIAP protein. The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be tested are contacted with each
                                             Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta; ds.
                                                                                                                                                                                                                                                                                                                                               Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein.
                                           inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 28-30; 43pp; Japanese.
                                                                                                                                                                                                                  98JP-00130378
                                                                                                                                                                                                                                                98JP-00130378
                                          X-linked
             Human XIAP coding sequence.
                                                                                                                                                                                                                                                                         (MATS/) MATSUMOTO K.
                                                                                                                                                                                                                                                                                                     WPI; 2000-078337/07.
                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY59451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as a drug
                                                                                                                                                           JP11326328-A.
                                                                                                                              Homo sapiens
                                                                                                                                                                                                                 13-MAY-1998;
                                                                                                                                                                                    26-NOV-1999
                                           Human;
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other and then the presence or formation of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta (Transforming growth factor-beta) type I and/or type II receptor Length 1659; Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other; Query Match

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120
                                                                                                                                                                         121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                          933
                                                                                                                                                   993
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                                                                                                                 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                               GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA
                                                                                  874 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
                                                      1 TAIGAAGCACGGAICGITACTITIGGAACAIGGAIATACTCAGITAACAAGGAGCAGCIT
                               ;
0
                             15; Indels
Score 173; DB 3;
Pred. No. 1.2e-49;
                            0; Mismatches
                                                                                                                                                                                                                                                                  ccaeciccaaararcr 1070
                                                                                                                                                                                                                                      CCAGGGTGCAAATACCT 197
87.4%;
92.4%;
          Best Local Similarity 92.4
Matches 182; Conservative
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BP.

ACA56455 standard; cDNA; 1659

ACA56455

06-JUN-2003 (first entry)

ACA56455;

HXXXH

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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of caray element in a microarray is particularly useful in the diagnostics and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, corensics and pharmacogenomics. The microarray is also useful for profiles for the effects of currently available therapeutic drugs. The compination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding to different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease companiations. Si diseases including pathway populations which can be used to diagnose to probe of the invention. Note: The sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not companiate directly from USPTO at Committee of the printed specification but was obtained in electronic constant and received the printed specification but was obtained in electronic constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant and constant an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide probes, useful as array elements in a monitoring the expression of a number of target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 173; DB 10;
Pred. No. 1.2e-49;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1053; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                    98US-00016434.
                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
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182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CCAGGGTGCAAATACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microarray for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Combination of
                                                                                                                                                                                                                   US6500938-B1
                                                                                                                                                                                                                                                                                                                    30-JAN-1998;
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                                                                                                                                                                                                                                                                   31-DEC-2002.
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TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT

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The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding at transducing comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray is useful in the control of cancer, an immunopathology or a nalso be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signaling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile continum pathology, e.g. AIDS, diabetes, pencreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. AIDS, diabetes, pencreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, epilepsy, Alzheimer's disease or depression. This sequence represents a chiman polynucleotide probe of the invention. Note: The sequence data for this pathor.
                                                                                                                                                                                                               Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cerrix; tumour; immunopathology; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 1053; 73pp; English.
                                                                                                                                                                           Human polynucleotide probe #1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seqdata.uspto.gov/sequence.html.
                                           ADIS6251 standard; DNA; 1659 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ;
                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                  22-APR-2004
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RESULT 9
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function
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                                                                                                                                                                                                                                                                                                                                                                              Neuroprotective, nootropic, transgenic fly; Alzheimer's disease, Abeta, amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy; gene; ds.
                                        120
                                                                                                 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                       New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protein of human homologue hCP35211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finelli AL, Freuler F, Konsolaki M;
                                                                                                                                                                                                                                                                                                                                                       DNA of APP related human homologue hCP35211.
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Protein of h
/note= "No start codon"
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                                                                                                                                                              CCAGGGTGCAATACCT 197
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14-JUN-2001; 2001US-0298309P.
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Reinhardt MWHM, Zusma
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P-PSDB; AA020511.
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Gaps

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Score 173, DB 12; Length 1659; Pred. No. 1.2e-49; 0; Mismatches 15; Indels 0:

87.4%; 92.4%;

Query Match
Best Local Similarity 92.4
Matches 182; Conservative

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947 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1006
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is a compound, triple helix DNA, antisense oligonucleotide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynucleotide sequence represents the DNA of the APP related human homologue hCP35211
                                                                                                                                                                                                                                                                                                                                                                                                                                886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2
                                                                                                                                                                                                                                                                                                                                                                                                             827 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Pred. No. 1.4e-49;
0; Mismatches 15; Indels
                                                                                                                                                                        Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 U; 0 Other;
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.4%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGGTGCAAATACCT
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genes (AAT70836-41) respectively code for a new class of mammalian proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap gene (for X-linked IAP gene) was isolated from a human foetal brain ZapII cDNA library using an X-linked sequence tag site that shows strong homology with the conserved ring zinc finger domain of baculovirus CpIAP mucleic acids can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene therapy)
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                                                                                                                                                                                                                                                                                                                                                                                                                    946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
                                                                                                                                                                                                                                                                                                                                     GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
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                                                                                                                                                                                                                                                                        1 TAIGAAGCACGGAICGTIACTTTTGGAACAIGGAIAIACTCAGTIAACAAGGAGCAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880; antisense; antiinfilammatory; cytostatic; tumour; ds.
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                                                                                                                                                                                                           Score 173; DB 2; Length 2540;
Pred. No. 1.4e-49;
                                                                                                                                                                            Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 0 U; 1 Other;
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92.48;
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Best Local Similarity 92.4
Matches 182; Conservative
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                  The present invention relates to antisense oligonucleotides designed to inhibit expression of the human X-linked inhibitor of apoptosis. The present sequence is the X-linked inhibitor of apoptosis DNA. Modified phosphorothicate 2'-methoxyethyl (2'-MOE) oligonucleotides are more effective inhibitors than unmodified oligonucleotides. The oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis expression in cells and tissues in vitro. The oligonucleotides are also useful for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to prevent infection, inflammation or tumour formation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; gene; antisense; inhibitor of apoptosis; HIAD1; HIAD2; XIAP; cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding inhibitor of apoptosis, XIAP #1.
                                                                                                                                                                             Score 173; DB 3;
Pred. No. 1.4e-49;
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                                                                                                                                                                                                      0; Mismatches
  Example 13; Col 43-48; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK93869 standard; cDNA; 2540 BP
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AEGERA THERAPEUTICS INC
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nes 182; Conservative
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, virtal pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945
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                                                   The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 173; DB 6; Length 25
Pred. No. 1.4e-49;
0; Mismatches 15; Indels
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Disclosure; Fig 1; 135pp; English
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antracycline-insensitive tumours, and classifying good and poor prognosis primary breast tumours. (I) is useful for large-scale molecular characterisation of breast cancer that help in prediction, prognosis and cancer treatment, and for detecting differentially expressed genes that
                     Novel polynucleotide library useful in molecular characterization of a carcinoma, comprising a pool of polynucleotide sequences or its subsequences which are either underexpressed or overexpressed in tumor
                                                            Claim 1; Page 289; 401pp; English.
                                                                                                                                                                                                                                                          correlated with a cancer
        WPI; 2002-619023/66.
                                                                                                                                                                                                                                                                                                       Matches 182;
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Target RNA; target RNA:support-attached test compound; flow cytometry; mass spectrometry; high-throughput screening; RNA motif; ss. X-linked inhibitor of apoptosis protein SEQ ID No 25. AAL53731 standard; RNA; 2540 BP (first entry) 07-FEB-2003 AAL53731; RESULT 15 

Homo sapiens

Search completed: October 22, 2004, 20:24:53

Job time

946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005 Identifying a test compound that binds to a target RNA molecule by separating the detectably labeled target RNA:support-attached test compound complex from uncomplexed target RNA molecules and test compounds by flow cytometry. The invention relates to a novel method for identifying a test compound that binds to a target RNA molecule comprising separating the detectably labeled target RNA: support-attached test compound complex from uncomplexed target RNA molecules and test compounds. The separating process is carried out by flow cytometry and determining a structure of the type of test compound of the RNA: support-attached test compound complex by mass spectrometry. The method is useful for high-throughput screening of libraries of compounds to identify pharmaceutical leads. This polymucleotide sequence represents one of the target RNA motifs/ GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 826 TATGAAGCACGGATCTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTT 886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA Gaps 0 Length 2540; Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 U; 0 Other; 15; Indels 87.4%; Score 173; DB 8; 92.4%; Pred. No. 1.4e-49; live 0; Mismatches 15; Example; Page 79-80; 131pp; English. 1006 ccasscracaararcr 1022 CCAGGGTGCAAATACCT 197 11-APR-2002; 2002WO-US011758. 11-APR-2001; 2001US-0282966P (PTCT-) PTC THERAPEUTICS INC. regions of the invention Matches 182; Conservative Similarity WPI; 2003-075534/07. WO200283837-A1 Almstead NG; 24-OCT-2002 121 61 181 Query Match Local ò 유 à qq 셤 ò à

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/cgn2 6/ptodata/1/ina/5B_COMB.seq:*
/cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-024-433-3
US-09-016-434-1053
US-08-511-485-3
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US-09-201-936-9
US-09-101-356-9
US-09-672-717-224
US-09-201-932-9
US-08-800-929A-9
US-08-800-929A-9
US-09-617-053A-9
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US-09-011-356-3
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Maximum Match 100%
Listing first 45 summaries
                                                           - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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US-09-128-155-17	US-09-3/9-8928-3/ US-09-016-434-1076	US-09-023-655-894	US-08-569-749-3	PCT-US96-12860-3	US-08-511-485-5	US-09-201-936-5	US-09-011-356-5	US-09-672-717-220	US-09-201-932-5	US-09-814-915A-31	US-09-205-144-1	US-09-814-915A-11	US-09-579-692B-7	US-09-212-971-5	US-08-800-929A-5	US-09-617-053A-5
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55.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4
109.6	76	16	16	16	16	16	16	16	96	9.	92	97	96	97	97	92
2 8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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100.0%; Score 198; DB 2; Length 2100; 100.0%; Pred. No. 2.9e-61; cive 0; Mismatches 0; Indels 0
                   Sequence 9, Application US/08511485
Partent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     SIAL.
STATE: MA
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION NUMBER: 07-540/002001
MARE: Clark, Paul T.
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELEPHONE: 617/542-8006
TELEPHONE: 617/542-8006
TELEPHONE: 617/542-8006
TELEPHONE: 617/542-8006
                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 198; Conservative
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STRANDEDNESS: both
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US-08-511-485-9
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US-09-672-717-224
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                                                                                                                                                             121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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                                                                                                                                   121 GGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 975
                                            61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                      976 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                      US-02-201-936-9, Application US/09201936

Patent No. 6541457
GENERAL INFORMATION:
APPLICANT: Koreluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
ITILE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES: AND OBTECTION METHODS
TITLE OF INVENTION: PROBES: AND OBTECTION METHODS
TITLE PREFERENCE: 10789/00303
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
BARLIER FILING DATE: 1998-02-04
BERLIER FILING DATE: 1998-02-04
BERLIER APPLICATION NUMBER: 08/576,956
BERLIER APPLICATION NUMBER: 08/511,485
BERLIER APPLICATION NUMBER: 08/511,485
BERLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 9

LENGTH: 2100

LENGTH: 2100

LENGTH: 2100
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US-09-011-356-9
; Sequence 9, Application US/09011356A
; Patent No. 6656704
; BENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1096 CCAGGGTGCAATACCTA 1113
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CORGANISM: Mus musculus
US-09-201-936-9
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916 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 975
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APPLICANT: Lighton, Peter
TITLE OF INVENTION: MAWALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REPERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT PILING DATE: 1998-09-14
CURRENT PILING DATE: 1996-09-15
EARLIER APPLICATION NUMBER: 00/576,956
EARLIER PILING DATE: 1995-10-22
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 224, Application US/09672717
Fatent No. 6673917
GENERAL INFORMATION:
APPLICANT: Accused, Robert G.
APPLICANT: Accused, Eric
APPLICANT: Accused, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025001
CURRENT APPLICATION NUMBER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 198; DB 4; Best Local Similarity 100.0%; Pred. No. 2.9e-61; Matches 198; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.9e-61;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ_ID NO 224
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Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-011-356-9
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US-08-800-929A-9
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                         1036 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1095
                                                                        121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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                                                                                                                                                                                                                                                                                                            GENERAL INCORMATION:
APPLICANT: Worneluk, Robert G.
APPLICANT: MacKenie, Alexander E.
APPLICANT: Bard Stephen
APPLICANT: Bard Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003004
CURRENT APPLICATION NUMBER: US/09/201,932A
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,366
EARLIER APPLICATION NUMBER: 09/011,366
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-10-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 455
NUMBER OF SEQ ID NOS: 455
ILENGTH . 2100
                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/09201932A
; Patent No. 6689562
                                                                                                                                                                         1096 CCAGGGTGCAAATACCTA 1113
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Best Local Similarity 100.
Matches 198; Conservative
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US-09-201-932-9
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US-09-212-971-9
; Sequence 9, Application US/09212971B
; Fatent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Baird, Stephen

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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Paat, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: DISBASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
CORRESPONDENCE ADDRESS: 17
CORRESPONDENCE ADDRESS: 17
CORRESPONDENCE ADDRESS: 17
CONTENT: Boston
STREET: 176 Federal Street
COUNTRY: USA
## AFFLICANT: Pratt, Christine
### APPLICANT: Pratt, Christine
### TITLE OF INVENTION: DETECTION AND MODULATION OF LAPS AND
### TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
### TITLE OF INVENTION: DETECTION
### CURRENT APPLICATION WUMBER: US/09/212,971B
### CURRENT APPLICATION WUMBER: 60/107,354
### EARLIER PILING DATE: 1996-12-16
### EARLIER PILING DATE: 1996-11-14
### EARLIER PILING DATE: 1996-11-14
### EARLIER PILING DATE: 1996-11-14
### EARLIER PILING DATE: 1997-02-13
### NUMBER OF SEQ ID NOS: 17
### SOFTWARE: FastSEQ for Windows Version 4.0
### SEQ ID NO 9
### IENGTH: 2691
### IENGTH: 2691
### IENGTH: 2691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.4%; Score 194.8; DB 3 99.0%; Pred. No. 4.7e-60; ive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTEN: DOS
SOFTWARE: FASTEN FOR Windows Version 2.0
CURRENY APPLICATION DATA:
FILLING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 9, Application US/08800929A; Patent No. 6133437
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Best Local Similarity 99.0
Matches 196; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Mus musculus
US-09-212-971-9
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Gaps

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                                                                                                                                                             1461 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT 1520
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                                                                                                                              GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                        1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Pred. No. 2.6e-52;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 63314103.
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT PILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
Indels
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BEDICANT: RODERT G. KOTNELUK et al.
TILLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TILLE OF INVENTION: MALE FERTILITY
TILLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/10/024,433
CURRENT FILING DATE: 2001-12-18
2;
Mismatches
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Patent No. 6797473
                                                                                                                                                                                                                                                                                                                                               1641 CCAGGGTGCAAATACCTA 1658
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Best Local Similarity 92.4
Matches 182; Conservative
  Matches 196; Conservative
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US-10-024-433-3
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Patent No. 6300492

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenale, Alexander E
APPLICANT: Baria, Stephen
APPLICANT: Baria, Stephen
APPLICANT: Baria, Stephen
APPLICANT: Baria, Stephen
APPLICANT: Baria, Stephen
APPLICANT: Baria MAD MODULATION OF IAPS AND
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/00903
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR APPLICATION NUMBER: US 08/800,929
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 194.8; DB 3;
Pred. No. 4.7e-60;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                     07891/009001
      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTOMNEY AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1641 ccadddrgcaaataccra 1658
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                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.4%;
99.0%;
                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.0
Matches 196; Conservative
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CRCANISM: Mus musculus
US-09-617-053A-9
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
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US-09-617-053A-9
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1 TATGAAGCACGGATCGTTACTT
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NAME: Clark Paul T.
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 0754
TELECOMONICATION INFORMATION:
TELEPHONE: 617/542-8976
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2540 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617/542-5077
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                               ; LIBRARY: GENBANK
; CLONE: 91016687
US-09-016-434-1053
            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-511-485-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1053, Application US/09016434
Fatent No. 560038
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: A174 PORTER DRIVE
STREET: CALIFORNIA
COUNTRY: USA
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                                                                                                                                                                           Query Match 87.4%; Score 173; DB 4; Length 1588; Best Local Similarity 92.4%; Pred. No. 2.6e-52; Matches 182; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
TELECOMONICATION INFORMATION:
TELECHONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1053:
SEQUENCE CHARACTERISTICS:
                NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1006 CCAGGGTGCAAATATCT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCAGGGTGCAAAIACCT 197
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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994 GGAGGGCTAACTGATTGGAAGCCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1053
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                                                                                                                 IGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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Query Match

87.4%; Score 173; DB 4; Length 1659;
Best Local Similarity 92.4%; Pred. No. 2.7e-52;
Matches 182; Conservative 0; Mismatches 15; Indels
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                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Malk, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCES: 38
CORRESPONDENCES: 38
CORRESPONDENCES: ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: DE PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.4%; Score 173; DB 2; I Best Local Similarity 92.4%; Pred. No. 3.3e-52; Matches 182; Conservative 0; Mismatches 15;
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GP: 07540/002001
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946 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 173; DB 4;
Pred. No. 3.3e-52;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Suan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESSS:
ADDRESSEE: INCYTE PHARRACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1996-02-05
EARLIER FILING DATE: 1996-05
EARLIER FILING DATE: 1995-12-22
EARLIER PELICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
$ SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: variation
LOCATION: (2540)
OTHER INFORMATION: N may be any nucleotide
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MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 182; Conservative
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
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US-09-023-655-900
                                                                                                                                                                                                                                                                                                          LENGTH: 2540
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APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIG
FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
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                                                              886 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGA 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander B.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09201936
Patent No. 6541457
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09392580 Patent No. 6087173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 ccadddracaararcr 1022
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                                                                                                                                                                                                                                                                                                                 181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (34)..(1527)
US-09-392-580-1
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US-09-201-936-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                 61
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CLASSIFICATION:

ATTORNEY/AGENT INPORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REGISTRATION NUMBER: PA-0001 US

REPERENCE/DOCKET NUMBER: PA-0001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 845-4166

INPORMATION FOR SEQ ID NO: 900:

SEQUENCE CHARACTERISTICS:

LENGTH: Z540 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

INMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 91184319
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Search completed: October 22, 2004, 22:14:06 Job time: 55 secs

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October 22, 2004, 21:14:39 ; Search time 242 Seconds (without alignments) 4192.299 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tatgaagcacggatcgttac.....acccagggtgcaaataccta 198
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2: /cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_BNW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PNW PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3407233 seqs, 2561960514 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 9. Annli			U,	Femiliary Seminary		ď.	Semience 3 Appli	ı			Sequence 331, App
SUMMARIES		ID	US-09-201-936-9	US-10-636-065-23	US-10-600-272-9	US-09-974-592-9	US-10-024-433-3	US-10-305-720-1	US-09-964-899-38	US-09-201-936-3	US-10-007-926A-	US-10-366-307-1	US-10-388-360-3	US-10-641-643-900
		DB	6	17	17	σ	13	16	6	6	15	15	15	16
	Query	Length	2100	2100	2100	2691	1588	1659	2404	2540	2540	2540	2540	2540
æ	Query	Match	100.0	100.0	100.0	98.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4	87.4
	(	Score	198	198	198	194.8	173	173	173	173	173	173	173	173
	Result	NO.	1	7	m	4	2	9	7	80	σ	10	11	12

13 173 87.4 2540 17 US-10-636-065-218 14 173 87.4 2540 17 US-10-636-065-231 15 173 87.4 2540 17 US-10-636-065-231 16 173 87.4 5232 9 US-10-636-065-231 18 147 75.3 1758 16 US-10-343-115-1 19 147.4 75.3 1758 16 US-10-343-115-1 19 147.4 75.3 1758 16 US-10-054-433-1 10 147.4 75.4 1559 13 US-10-055-407-16 2 1 109.6 55.4 176373 13 US-10-055-407-16 2 2 776 38.4 2563 16 US-10-05-54-906 2 2 776 38.4 2563 16 US-10-25-24-906 2 6 76 38.4 2563 16 US-10-636-065-22 2 7 6 38.4 2676 17 US-10-636-065-22 2 7 7 8 38.4 2676 17 US-10-636-065-22 2 7 7 8 38.4 2676 17 US-10-636-065-22 2 7 7 8 38.4 2676 17 US-10-636-065-22 2 7 7 8 38.4 2676 17 US-10-636-065-22 2 7 7 8 38.4 2676 17 US-10-776-827-31 2 7 8 38.4 2676 17 US-10-776-827-31 2 7 8 38.4 2676 17 US-10-776-827-31 2 7 8 38.4 3076 17 US-10-197-26-115 2 7 8 38.4 3076 17 US-10-197-26-115 2 8 8 3 3 3 3 6 15 US-10-388-263-157 3 8 4 3076 15 US-10-388-263-157 3 8 4 3076 15 US-10-388-263-157 3 8 4 3165 15 US-10-269-909-5 4 7 8 38.4 3165 15 US-10-342-3461-7 2 8 4 3 3 6 5 15 US-10-342-3461-7 2 8 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 4 5857 15 US-10-342-817-76 3 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
13 173 87.4 2540 15 173 87.4 2540 16 173 87.4 2540 17 149 75.3 1758 19 147.4 74.4 152331 22 776 38.4 2563 24 76 38.4 2563 25 76 38.4 2676 29 76 38.4 2676 31 76 38.4 2676 31 76 38.4 2676 32 76 38.4 2676 33 76 38.4 3076 34 76 38.4 3076 35 76 38.4 3076 36 76 38.4 3076 37 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3076 38 76 38.4 3165 41 76 38.4 3165 41 76 38.4 5844
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1144 1165 1170 1170 1170 1170 1170 1170 1170 117

## ALIGNMENTS

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Sequence 9, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT FILING DATE: 1998-12-01
FEARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,366
EARLIER PILING DATE: 1996-02-04
EARLIER PILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FREESEQ for Windows Version 3.0
TYPE: DNA
ORGANISM: Wus musculus
US-09-201-936-9
Query Match
Best Local Similarity 100.0%; Score 198; DB 9; Length 2100; Best Local Similarity 00.08; Mismatches 0, Indels 0, G
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1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT 6

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Sequence 9.74-592-9

Sequence 9. Application US/09974592

Patent No. US20020120121A1

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G

APPLICANT: MacKenzie, Alexander E

APPLICANT: Baird, Stephen
APPLICANT: Tanny Berter

APPLICANT: Tanny Berter

APPLICANT: Tanny Berjamin K

APPLICANT: Tanny Berjamin K

APPLICANT: Tanny Berjamin K

APPLICANT: Tanny Berjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DISEASE

TITLE OF INVENTION: DISEASE

FILE REFERENCE: 07891/009004

CURRENT PILING DATE: 2001-10-09

PRIOR PRILIG DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/617,053

PRIOR APPLICATION DATE: 2000-07-14

PRIOR APPLICATION DATE: 2000-07-14

PRIOR APPLICATION DATE: 2000-07-14

PRIOR PRILING DATE: 1999-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1036 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 2100;
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99.0%; Pred. No. 4.6e-57;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 198; DB 17; Best Local Similarity 100.0%; Pred. No. 3.1e-58; Matches 198; Conservative 0; Mismatches 0;
FILE REFERENCE: 07891/003006
CURRENT APPLICATION WUMBER: US/10/600,272
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1998-02-04
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1996-05
PRIOR PILING DATE: 1995-12-22
PRIOR PILING DATE: 1995-12-22
PRIOR APPLICATION NUMBER: US 08/511,485
PRIOR FILING DATE: 1995-08-04
NUMBER: OF SEQ ID NOS: 45
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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Best Local Similarity 99.0
Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
US-10-600-272-9
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100.0%; Score 198; DB 17; Length 2100;
Best Local Similarity 100.0%; Pred. No. 3.1e-58;
Matches 198; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 224, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Rorneluk, Robert G.
APPLICANT: LaCasse, Bric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; ITILE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; ITILE OF INVENTION: Thereof
; ITILE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION: Thereof
; TITLE OF INVENTION UNMBER: 09/672,717
; PRIOR APPLICATION NUMBER: 09/672,717
; PRIOR APPLICATION NUMBER: 09/672,717
; ROFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1096 CCAGGGTGCAAATACCTA 1113
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US-10-636-065-224
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LENGTH: 2100
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Fatent No. US20020174446A1
GENERAL INFORMATION:
APPLICANT: Cohen, Dalla et al.
ITILE OF INVENTION: Identification of Genes Involved in
ITILE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster:
FILE REFERENCE: 4-31612 A
CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/298,309
PRIOR APPLICATION NUMBER: 60/298,309
PRIOR APPLICATION NUMBER: 60/298,309
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                                                                                                        NAME/KEY: misc feature; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1016687
US-10-305-720-1053
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Pred. No. 1.5e-49;
0; Mismatches 15;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 2404
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Best Local Similarity 92.4%;
Matches 182; Conservative
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                   LENGTH: 1659
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 182; Conserv
SEQ ID NO 1053
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TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR PAPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGram
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                1461 TATGAAGCACGGATCGTTACTTTTGGAACATGGACATCCTCAGTTAACAAGGAGCAGCTT
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                                                                            GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
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TITLE OF INVENTION: MALE FERTILITY
TITLE OF INVENTION: MALE FERTILITY
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/10/024,433
CURRENT APPLICATION NUMBER: 09/239,867
FRIOR APPLICATION NUMBER: 09/239,867
FRIOR APPLICATION NUMBER: 09/239,867
RRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 10
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Pred. No. 1.5e-49;
0; Mismatches 15;
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; Publication No. US20040010136A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         1641 CCAGGGTGCAAATACCTA 1658
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Publication No. US20020086409A1
GENERAL INFORMATION:
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Best Local Similarity
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87.4%; Score 173; DB 9; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15; Indels
                                                                                                                APPLICANT: MacKenzie, Alexander G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Jaston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE APPLICATION NUMBER: 09/011,356
CURRENT APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
FEARLIER PAPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
FEARLIER PAPLICATION NUMBER: 08/576,956
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NAME/KEY: variation
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OTHER INFORMATION: (2540)
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NUMBER OF SEQ ID NOS: 45
SEQ ID NO 3
Sequence 3, Application US/09201936 Publication No. US20020187946A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-007-926A-274
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1005
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; Sequence 1, Application US/2030224399A1
; GENERAL INFORMATION:
; APPLICANT Reed, John C.
; TITLE OF INVENTION: Freed, John C.
; TITLE OF INVENTION: For Patients with a Prostate Neoplastic Condition
; TITLE OF INVENTION: More Patients with a Prostate Replacation NUMBER: US/10/366,307
; CURRENT APPLICATION NUMBER: US/10/366,307
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 60/356,956
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 1
; SEQ ID NO 1
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                                                                                                                                                                                                         CTHER INFORMATION: baculoviral iap repeat-containing 4 (BIRC4); OTHER INFORMATION: gene.

US-10-007-926A-274
                                                                                                                                                                                                                                                                                                                Length 2540;
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92.4%; Pred. No. 1.8e-49;
live 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                   Score 173; DB 15;
Pred. No. 1.8e-49;
0; Mismatches 15;
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PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 274
LENGTH: 2540
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.4
Matches 182; Conservative
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Matches 182; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-636-065-218
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Sequence 331, Application US/10388360

Publication No. US200302255281

GENERAL INFORMATION:

APPLICANT: GENOMIC HEALTH

APPLICANT: Cronin, Maureen T.

APPLICANT: Shak, Steve

APPLICANT: Shak, Steve

APPLICANT: Shak, Steve

APPLICANT: Shak, Steve

APPLICANT: Shak, Steve

APPLICANT: Walker, Michael C.

APPLICANT: Shak, Steve

APPLICANT: Walker, Michael C.

PREMEMY OF INVENTION GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES

CURRENT PRILING DATE: 2070-001US

CURRENT FILING DATE: 2002-09-18

PRIOR PLILOR INDMERS: US 60/412,049

PRIOR PLILOR INDMERS: US 60/364,890

PRIOR PLILOR DATE: 2002-09-18

PRIOR PLILOR DATE: 2002-09-18

PRIOR PLILOR DATE: 2002-09-18

SOFTWARE: PRESSEQ for Windows Version 4.0

LENGTH: 2540
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Susan G. Stuart
Susan G. Stuart
Jeslihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.4%; Score 173; DB 15;
92.4%; Pred. No. 1.8e-49;
live 0; Mismatches 15;
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 900, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.4;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Homo sapiens US-10-388-360-331
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946 GGAGGCTAACTGATTGGAAGCCCAGTGAAGACCTTGGGAACAACATGCTAAATGGTAT 1005
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92.4%; Pred. No. 1.8e-49;
tive 0; Mismatches 15; Indels 0
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Publication No. US20040127694A1

GENERAL INFORMATION:
APPLICANT: Rorneluk, Robert G.
APPLICANT: LaCase, Exic
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Woung, Sean
TITLE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE REFERENCE: 07991/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT APPLICATION NUMBER: 09/672,717
PRIOR PILING DATE: 2000-09-28
NUMBER OF EXC ID NOS: 231
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 218
LENGTH: 2540
                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRAATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: g1184319
SEQUENCE DESCRIPTION: SEQ ID NO: 900:
                            APPLICATION NUMBER: US/10/641,643
                                               FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2540 base pairs
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STRANDEDNESS: single
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
LIBRARY: GENBANK
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US-10-636-065-231
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                                                                   Length 2540;
                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MORGELIE, ALEXANDER E.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MARMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REPERENCE: 07891/03006
CURRENT APPLICATION NUMBER: US/10/600,272
CURRENT APPLICATION NUMBER: US/01/0400,272
CURRENT APPLICATION NUMBER: US/01/0400,272
PRIOR PILING DATE: 1998-02-04
PRIOR PILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                      Query Match

87.4%; Score 173; DB 17;
Best Local Similarity 92.4%; Pred. No. 1.8e-49;
Matches 182; Conservative 0; Mismatches 15;
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OTHER INFORMATION: N may be any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccasserschartrer 1022
OTHER INFORMATION: n=a,t,c, or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGTGCAAATACCT 197
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     ; OTHER INFORMAT
US-10-636-065-218
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1602 GGAGGGCTAACTGATTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTAT 1661
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                                                                                                                                                            Sequence 211, Application US/10636065

Sequence 211, Application US/10636065

Publication No. US20040127694A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Young, Sean

TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses

TITLE OF INVENTION: Thereof

FILE REFERENCE: 07891/025005

CURRENT FILING DATE: 2003-08-07

PRIOR APPLICATION NUMBER: 09/672,717

PRIOR PLILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 231

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.9e-49;
0; Mismatches 15;
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                                 1006 CCAGGGCAATATCT 1022
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181 CCAGGGTGCAAATACCT 197
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Best Local Similarity 92.4%;
Matches 182; Conservative
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ORGANISM: Homo sapiens
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October 22, 2004, 20:10:53 ; Search time 1727.5 Seconds (without alignments) 4176.594 Million cell updates/sec
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198
1 tatgaagcacggatcgttac.....acccagggtgcaaataccta 198
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                               32822875 seqs, 18219865908 residues
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                                                              OM nucleic - nucleic search, using sw model
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2: gb estl: *
4: gb est2: *
5: gb est2: *
6: gb est4: *
7: gb est5: *
7: gb est5: *
9: gb gss2: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	CD350728 III-M-GIO-	۰.	-					-		-					_				CE100865 tigr-gss-	BU658508 C137a11 7		~	_	•
SUMMARIES	í	1.0	CD350778	AI573382	CN315131	BC056914	BC046168	BB663325	BB650856	BF659610	BM220130	BQ552032	BM805359	AU123207	CF222542	BY662508	BZ242580	AV706807	AY398945	AY398943	CE100865	BU658508	AW375598	AW375594	AW846507	AW375599
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38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.0	37.8	37.6	37.6	37.1	36.6	36.0	35.6	34.9	34.8	34.5	34.3
91	92	16	16	92	92	94	92	16	75.2	74.8	74.4	74.4	73.4	72.4	71.2	70.4	69.2	69	68.4	68
25	26	27	c 28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	C 44	45

## ALIGNMENTS

CD350778  UI-M-GIO-cgh-g-23-0-UI.rl NIH_BMAP_GIO Mus musculus cDNA clone INAGB:6853392 5', mRNA sequence. CD350778  CD350778.1 GI:31142365 EST. Mus musculus (house mouse)	Mus musculus musculus to the budaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 773)  National 1 to 773)  National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  Email: Gapbs-r@mail.nih.gov, Tissue procurement: Dr. Jum Lin, University of Iowa Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov Tissue procurement: Dr. Jum Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project	0,
RESULT 1 CD350778 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	OKGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUTCE

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/tissue_type="embryonic stem cells, cell lines H1, H7, and
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                                                                                                                                                                                                                                                                                          GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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                                                                                                                                                                                                             61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
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                                                                                                                                                                                                                                                                                                                1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT
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17000417981828 GRN_ES Homo sapiens CDNA 5', mRNA sequence
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                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 533 5td Error: 0.00.
                                                        Score 168; DB 1;
pred. No. 6.5e-43;
0; Mismatches 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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CN315131.1 GI:47331545
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larity 93.4%;
Conservative
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Best Local Similarity
Matches 172; Conserv
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sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (Dass 1 to 628)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
The Wash Uron, R. and Wilson, R.
The Wash Uron Mouse EST Project 1999
Unpublished (1999)
Contact: Marra Myash Urol Mouse EST Project 1999
Washington University, School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                      GATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCA
                                                                                                                                                                                                                                           11 GGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTG
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                                                                                                                                                                                                       Gaps
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                                                                                                                                                               Score 176.8; DB 6; Length 773; Pred. No. 1e-45;
                                                                                                                                                                                                       Indels
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/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 440.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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Query Match
Best Local Similarity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ratcheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, S.J., Bosak, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanochez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smilus, D.E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                            BC056914 1851 bp mRNA linear HTC 25-JUN-2004 HOMO sapiens baculoviral IAP repeat-containing 8, mRNA (cDNA clone IMAGE:5742924), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                       121 GGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTAC 180
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215 TCAAGAGCTGGATTTTATGCTTTAGGTGAAAGGTAAAGTAAAGTGCTTTCACTGTGGA 274
                                                                                                      275 GGGGGGCTAACTGGATTGGAAGCCCAGCGAAGACCCTTGGGAAACAACATGATAAATGGCAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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DNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                       181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC056914.1 GI:34784469
                                                                                                                                                                                                                               335 CCAGGGTGTAAATATCT 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web Site: http://www.shgc.stanford.edu
Series: IRAK Plate: 119 Row: h Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16974127 This clone has the following problem: retained intron. Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1789)
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Submitted (31-5AM-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1062 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTACTCCGTTAACAAAGAGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.3%; Score 149; DB 3; Length 1851; 84.8%; Pred. No. 1.2e-36; 1.ve 0; Mismatches 30; Indels
                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742924"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH MGC_119"
/lab_host="DH10B"
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Contact: MGC help desk
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                                                                                                                                                                                           /organism="Homo sapiens"
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231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.jp, URL.http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                         1 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: frame shifted.
Location/Qualifiers
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                                                                                                                                                                                                                                                          DB 3; Length 1789;
                                                                                                                                                                                                                                                                                          31; Indels
                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742590"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
                                                                                                                                                                                                                                                          Score 147.4; DB 3
Pred. No. 3.8e-36;
0; Mismatches 31
                                                                                                                                                                                                         note="Vector: pCMV-SPORT6"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGTGCAAATACCT 197
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                                                                                                                                                                                                                                                            74.48;
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                                                                                                                                                                                                                                                                                             Matches 166; Conservative
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BB663325
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a norredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aisawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational halysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BB650856.1 GI:16485110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 TTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGGCTCACGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 15 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                    Matesuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., inoue,Y., Arland Hayashizaki,Y.
and Hayashizaki,Y.
RIKBN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·,
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Best Local Similarity 91.9%; Pred. No. 1.4e-23;
Matches 114; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="15 days embryo"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="D930039G22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e mouse tissues.
Location/Qualifiers
1..617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue_type="head"
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REFERENCE AUTHORS

COMMENT

KEYWORDS

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/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF659610.1 GI:11924744
                                                                                                            52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                   Similarity
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Matches 105; Conserv
                                                                                                                                                          Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
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                                                                                                              Query Match
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KEYWORDS
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                                                           ORIGIN
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               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 504)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,T.,
Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Takeda,Y., Tanaka,T., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegac.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muzmatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare [ill-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1611-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yomeda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-1884-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDMA library. Genome Res. 11 (2), 281-289 (2001) KOndo, S., Shinagawa, A., Saico, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ayashizahi,:
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/lab_host="DH10B"
/clone lib="RIKEN full-length enriched, 0 day neonate
cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Sire 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y.,
Konno, H., Fukunishi, Y.,
Sugahara, Y. and Hayashizaki, Y.
Computer based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="cerebellum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
|db_xref="taxon:10090"
|clone="C230036005"
                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
Mus musculus (house mouse)
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                       ORGANISM
                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
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FEATURES

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uz88el2.x1 NCI CGAP Lu29 Mus musculus CDNA clone IMAGE:3676174 3' similar to SW:IAP3_MOUSE Q60989 INHIBITOR OF APOPTOSIS PROTEIN 3;, mRNA sequence.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                       GGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="spontaneous tumor, metastatic to mammary. Stem cell origin."

Alab host="nH108"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AGCAGCTIGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                   207 GGNGAAGGCGATAAAGTGAAGTGCTTTCACTGGGGAGGAGGAGGCTCACGGATTGGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                       145 AGTGAAGACCCTGGGACCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGAAGACCCTTGGGAACAGCATGCGAAGTGGTACCCAGGGTGCAAATACCTA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0:
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                                                                                                                                                                 Length
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                    ;
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                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%; Score 100.8; DB 2; 93.8%; Pred. No. 2.4e-21; live 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: polyT not found Seq primer: -400P from Gibco High quality sequence stop: 226.

Location/Qualifiers
                                                                                                                                                                 Score 103.4; DB Pred. No. 4e-22;
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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/clone="IMAGE:3676174"
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584 bp mRNA linear EST 20-JUN-2002
H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4013A06 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4013 row: A column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 TTAGGTGAAGGCGATAAAGTGAAGTGCTTTCACTGTGGAGGAGGAGGCTCACGGATTGGAAG 201
                                                                                                                                                                        TTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases 1 to 584)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Asrgull, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S. H. Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set
                                                                                                                                                                                                                           260 TTAGGTGAAGGCGATAAAGTGAAGTGCTTTCACTGTGGAGGAGGGCTCACGGATTGGAAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This
clone is among a rearrayed set of 7,407 clones from more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                          Gaps
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0
                                                                                                                                                                                                                                                                                                             142 CCAAGTGAAGACCCTGGGACCAGCATGCTAAGTGCTACCCAGGGT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 584;
                                                                        Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                          5; Indels
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al Similarity 95.3%; Score 98; DB 5; Lei
al Similarity 95.3%; Pred. No. 2.3e-20;
101; Conservative 0; Mismatches 5;
                                                                          DB 4;
2e-20;
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                                                                                                                        0; Mismatches
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/mol_type="mRNA"
/strain="C57BL/6"
                                                                          Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: H4013 row: A column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 584
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than 20 cDNA libraries.
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/clone="H4013A06"
by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ552032
BQ552032.1 GI:21452918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other EST8: H4013A06-5
Contact: Yong Qian
Laboratory of Genetics
                                                                          49.5%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="mixed"
                                                                                                                             Conservative
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BQ552032/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Essue type="Male genital ridge/mesonephros"
/ Lissue type="Male genital ridge/mesonephros"
/ Lab_hoft="Mula Mouse 12.5-dpc Male Genital
/ Lone lib="Mula Mouse 12.5-dpc Male Genital
/ Lone lib="Mula Mouse 12.5-dpc Male Genital
Ridge/Mesonephros cDNA Library (Long)"
Ridge/Mesonephros cDNA Library (Long)"
Roti; Mouse cDNA project by the Laboratory of Genetics,
Noti; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Dases 1 to 334)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                   EST 07-JUN-2003
                                                                                                                                                                                                334 bp mRNA linear EST 07-JUN-2005
C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA
Library (Long) Mus musculus cDNA clone NIA:C0935E08 IMAGE:30037975
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AGCAGCTIGCAAGAGTIGGAITITAAGCITIAGGIGAAGGCGAIAAAGICAAGIGCITIC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Dec 14, 2001 this sequence version replaced gi:17780130. Contact: Dawood B. Dudekula Laboratory of Genetics National Institutes of Health Smail: casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@1gsun.grc.nia.nih.gov
Plate: C0935 row: E column: 08 Seq primer: -21M13 Forward
High quality sequence stop: 334
POLYA=Yes.
                                                                                  ACTGTGGAGGAGGCTCTCGGATTGGAAGCCAAGTGAAGACCCTTGGGAACA 206
                                                        ACTGTGGAGGAGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGGACCA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .334

/organism="Mus musculus"

/mol type="mRNA"

/strain="C57BL/6J"

/db xref="miasEr:C035E08-3"

/db xref="taxon:10090"

/clone="NIA:C0935E08 IMAGE:30037975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 11 (9), 1553-1558 (2001)
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Mus musculus
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us-09-654-743-51.rst

DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 11 BM805359

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ORGANISM

SOURCE

TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

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CF222542
AGENCOURT_14926978 NICHD_XGC_Embs Xenopus tropicalis cDNA clone
IMAGES6981334 5', mRNA sequence.
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y., Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Suzuki, Y., Kawai, Y., Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NT2RM1"
/note="Vector: pUC19FL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 GGTGAAGGTGATAAAGTACATTTCACTGTGGAGGANGGCTAACTGATTGGAAGCCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Genomics
Bidg. 31 RmioADAT Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Paregaration: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                            Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
TTE1: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%; Score 90.2; DB 1;
86.7%; Pred. No. 7.3e-18;
vative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="NT2RM1000921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF222542.1 GI:33423250
                                                                                                                                                                                                                                                                        Contact: Takao Isogai
Genomics Laboratory
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                            Homo sapiens
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics
                                                                                                                                                                                                         BM805359 1177 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU123207 S36 bp mRNA linear BST 01-AUG-2002 AU123207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAML274 row: m column: 06
High quality sequence stop: 409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.6%; Score 92.2; DB 4; Length 1177;
llarity 88.5%; Pred. No. 2e-18;
Conservative 0; Mismatches 13; Indels 0;
                       187
                                              200 CCAAGTGAAGACCCTTGGGAACAGCATGCGAAGTGGTACCCAGGGT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                 142 CCAAGTGAAGACCCCTGGGACCAGCATGCTAAGTGCTACCCAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5728685"
/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                       BM805359.1 GI:19122182
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                5', mRNA sequence.
BM805359
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AU123207.1
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Best Local 8
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source

FEATURES

DEFINITION

RESULT 12 AU123207

Matches

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ORIGIN

ACCESSION VERSION

KEYWORDS

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Gaps

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Length 536;

144

us-09-654-743-51.rst

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"I (bases 1 to 373)

I (bases 1 to 373)

S (Aczaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yamanaka,I., Nikaido,I., Osato,N., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., BatalovyS., Basela,K.W., Blake,J.A., Bradt,D.P., Brusic,V., Corbani,L.B., Ccusins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pertea,G., Pertovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="gastrula"
/dev stage="embryo, stages 10-13"
/dev stage="embryo, stages 10-13"
/lab_nost="DH10B (plage-resistant)"
/clone lib="WIGHD XGC Embs"
/note="Wector: pCWV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.0 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 16-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAGTGAAGTGCTTCCACTGTGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov. f column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTTAACAAGGAGCAGCTT
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BY662508 RIKEN full-length enriched, 14.5 days embryo RP+/+
Rathke's pouches Mus musculus cDNA clone K720015L24 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88.2; DB 6;
Pred. No. 3.6e-17;
                                                                                                                                                                                                                                                           /organism="Xenopus tropicalis"
| mol_type="mRNA"
| db xref="taxon:8564"
| clone="IMAGE:6981334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                  High quality sequence start: 3
High quality sequence stop: 735.
Location/Qualifiers
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Mus musculus
Eukaryota; Metazoa; Chordat
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BY662508.1 GI:27033688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCAGGGTGCAAATACCT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 CCTGGATGCAAGTTCCT 463
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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Watanabe, Y., Watanabe, Y., Wallestedt, C., Watanabe, Y., Watanabe, Y., Wallestedt, C., Wang, Y., Watanabe, Y., Wang, I., Yang, I., Yang, I., Yang, I., Yang, I., Sang, I., Yang, I., Sang, I., Sang, I., Sang, I., Sang, I., Sang, I., Kanai, J., Alzawa, K., Sakazume, N., Hirozane-Kishikawa, T., Kawai, J., Alzawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Itoh, M., Kagwa, I., Miyazaki, J., Waki, K., Sasaki, D., Shibata, K., Shinagawa, I., Wayazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, J., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ocontact: Yoshinde Hayashizaki.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa, K., Akimura, T., Arakawa, T., Carhinci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Komno, H.,
Miyazaki, A., Murataa, M., Nakamura, M., Nomura, K., Numazaki, R.,
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Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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genes. Genome Res. 10 (10), 1617-1630 (2000)
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
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/dev_stage="14.5 days embryo RP+/+"
/clone_lib="RIKEN full-length enriched, 14.5 days embryo
RP+/+ Rathke's pouches"
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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94.4%; Pred. No. 7.1e-17;
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/db_xref="taxon:10090"
/clone="K720015L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
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Shvartsbeyn, A., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 Mbol segment
Unpublished (1999)
Chter GSSs: CH230-252Dl.TJ
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat220.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                                                                                                              849 bp DNA linear GSS 12-OCT-2002 CH330-552D1.TVB CHORI-230 Segment 2 Rattus norvegicus genomic clone BZ242580
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 252 row: D column: 1 Seq primer: 17 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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/call type="Brain"
/clone lib=-1230 Segment 2"
/note="Vector: pTARRAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SENHSd/MCW) BAC library produced by
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    .849
    organism="Rattus norvegicus"

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/strain="BN/SsNHsd/MCW"
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/clone="CH230-252D1"
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AUTHORS
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Claim 27; Page 79-80; 219pp; English
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N-PSDB; AAT70839.
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ADK34975
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AAE00367
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## ALIGNMENTS

apoptosis polypeptide - used to patients, and for detection of Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis. Liston P; 438. .483 /label= Ring\_zinc\_finger Nucleic acid encoding an inhibitor of inhibit apoptosis in e.g. HIV or AIDS susceptibility to apoptotic disease. Baird S, Location/Qualifiers AAW19584 standard; protein; 496 AA Mouse apoptosis inhibitor M-XIAP. 163. .230 /label= BIR-2 264. .329 /label= BIR-3 26. .93 /label= BIR-1 96WO-IB001022. 95US-00511485. Mackenzie AE,

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Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2 (AAM19581-86) are a new class of mammalian proteins that are inhibitors of apoptosis (IAP) and which are characterised by the presence of a ring zinc finger domain (see also AAM19587) and at least one BIR (baculovirus was deduced from the m-xiap gene (AAP70839) isolated from a mouse embryocon library. The IAP olypeptides can be expressed in host cells (in involving apoptosis, esp. in a human diagnosed as HIV-positive or as having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or ischemic injury, seleted from myocardial infarction, stroke, reperfusion injury, or a toxin-induced liver disease
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AAW69297 standard; protein; 496 AA.
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apoptosis protein; apoptosis enhancer; NAIP polypeptide; e disease; IAP; therapy; cancer; mouse; XIAP protein.

WO9835693-A2

20-AUG-1998

98WO-IB000781. 13-FEB-1998; 13-FEB-1997;

97US-00800929. (UYOT-) UNIV OTTAWA.

Korneluk R,

Inducing apoptosis in proliferative mammalian cells with inhibitor of or NAIP polypeptide - also methods for prognosis based on presence of and NAIP, specifically applied to cancers involving p53 mutations. WPI; 1998-467164/40. N-PSDB; AAV55041.

'n, Tsang

Baird S,

Liston P,

Mackenzie AE,

Disclosure; Fig 4; 147pp; English.

This sequence is the murine XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyroid, central nervous system, prostate, colon,

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rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors
                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                               Mouse; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection;
                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of equal apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptocic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative
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                                                                                                                                                                        Length 496;
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                                                                                                                                                                   Score 386; DB 2;
Pred. No. 1.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holcik M,
                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       ABG65666 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse inhibitor of apoptosis, XIAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baird S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 12; Fig 4; 135pp; English.
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                                                                                                                                                                  100.0%;
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                                                                                                                                                                               Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative disease.
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                                                                                                                                                                                                                                                                                        61 PGCKYL 66
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                                                                                                                                Sequence 496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200226968-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG65666;
                                                                                                                                                                Query Match
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Matches
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                                          adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a mouse IAP
                                                                                                                                                                                                                                             This invention relates to a substantially pure polypeptide having a length of less than 100 amino acids and capable of forming a complex with a polypeptide that includes a baculovirus inhibitor of apoptosis repeat (BIR) domain. The apoptosis pathway is known to play a critical role in
                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide capable of forming a complex with a polypeptide comprising a baculovirus inhibitor of apoptosis repeat domain useful for treating cancer and other neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer,
                                                                                                                                                                                                                            1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small cell lung carcinoma; uterine cancer; renal cell carcinoma;
                                                                                                                                                                                                     0;
                                                                                                                                                                        Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
                                                                                                                                                                                                   Indels
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                                                                                                                                                                      100.0%; Score 386; DB 5;
100.0%; Pred. No. 1.9e-39;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilm's tumour; BIR 3 domain; mouse; murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korneluk RG, La Casse E,
                                                                                                                                                                                                                                                                                                                                                                           ADB61828 standard; protein; 66 AA.
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                                                                                                                                                                                   Local Similarity 100.
nes 66; Conservative
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                                                                                                               protein sequence
                                                                                                                                         Sequence 496 AA;
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                                                                                                                                                                     Query Match
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embryonic development, viral pathogenesis, cancer, autoimmune disorders

and neurodegenerative diseases. The failure of the apoptotic response has

been implicated in the development of cancer, autoimmune disorders (for

example systemic lupus erythematosis and multiple sclerosis) and viral

infections (including herpes virus, poxvirus and adenovirus. The

infections (including herpes virus, poxvirus and adenovirus. The

chibilitors of apoptosis (IAPs) are a family of proteins possessing one or

more baculovirus IAP repeat (EIR) domains. Human IAPs, XIAP, HIARI

(cIAP2) and HIAP2 (CIAP1) all posses three BIR domains and carboxy

terminal RING zinc fingers. The IAPs bind and inhibit caspases -3, -7 and

-9 which are proteases involved in the initiation of apoptosis. Compounds

which inhibit the activity of IAPs may therefore have cytostatic activity

through the enhancement of apoptosis. The polypeptides of the invention

are candidate peptide ligands for binding to the BIR domain of IAPs. They

may be useful for the treatment of cancer, uterine cancer, testicular

cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma

cand Willin's tumour, and for enhancing apoptosis: The present sequence is

that of the mouse inhibitor of apoptosis (IAP) protein XIAP BIR3 domains

which was used to demonstrate homology to human IAP protein BIR domains

concer, which the peptides of the invention are targeted to bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of murine inhibitor of apoptosis protein MIAP3. The invention provides a nucleic acid, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibitor of apoptosis; MIAP3; mouse; apoptosis; cancer; leukaemia;
lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YEARIVIFGTWISSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 372; DB 7; Length 66;
Pred. No. 1e-38;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse inhibitor of apoptosis protein MIAP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 15A; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP72157 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.4%;
97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 YEARIVIFGIWISSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY 323
an antisense oligonucleotide, which specifically hybridises to a nucleic acid encoding an inhibitor of apoptosis protein, especially MIAP2, MIAP2, MIAP3, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to treat acute lymphorytic leukaemia, acute myelogenous leukaemia, ung cancer, breast cancer, ovarian cancer, prostate cancer, lymphona, Hodgkin's disease, malignant melanoma, neuroblastoma, renal cell carcinoma and squamous cell carcinoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  baculovirus inhibitor of apoptosis repeat domain; BIR domain; apoptosis pathway; embryonic development; viral pathogenesis; cancer; autoimmune disorder; neurodegenerative disease; apoptotic response; systemic luque erythematosis; multiple sclerosis; viral infection; herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; KIAP; HIAPP; CIAPI; RIAP; AIAPP; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; RIAPI; CIAPI; CIAPI; RIAPI; CIAPI; CIAPI; RIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; CIAPI; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                      Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003040172-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003
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ADB61827
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been implicated in the development of cancer, autoimmune disorders (for example systemic lupus erythematosis and multiple sclerosis) and viral infections (including herpes virus, poxvirus and adenovirus. The infections (including herpes virus, poxvirus and adenovirus. The inhibitors of apoptosis (IAPS) are a family of proteins possessing one or more baculovirus lap repeat (BIR) domains. Human laps, XIAP, HIAP1 (CC (CIAP2) and HIAP2) and HIAP2 (CIAP4) all posses three BIR domains and carboxy terminal RING zinc fingers. The laps bind and inhibit caspases -3, -7 and through the activity of IAPS may therefore have cytostatic activity through the enhancement of apoptosis. The polypeptides of the invention are candidate peptide ligands for blinding to the BIR domain of IAPS. They cancer, small cell light carcinoma, cervical cancer, uterine cancer, testicular cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma and whilm's tumour, and for enhancing apoptosis. The present sequence is that of the rat inhibitor of apoptosis to human IAPP protein BIR domains which was used to demonstrate homology to human IAPP protein BIR domains.
                       embryonic development, viral pathogenesis, cancer, autoimmune disorders and neurodegenerative diseases. The failure of the apoptotic response has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY 60
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The apoptosis pathway is known to play a critical role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             baculovirus inhibitor of apoptosis repeat domain; BIR domain; apoptosis pathway; embryonic development; viral pathogenesis; cancer; autoimmune disorder; neurodegenerius disease; apoptocic response; systemic lupus erythematosis; multiple sclerosis; viral infection; herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAPP; XIAP; HIAPI; cIAP2; HIAP2; cIAP1, RING zinc finger; caspase-3; caspase-7; carapase-9; cytostatic; neoplasm; leukaemia; colon carcinoma; cervical cancer; uterine cancer; testicular cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       small cell lung carcinoma; uterine cancer; renal cell carcinoma; Wilm's tumour; human; BIR 3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.8%; Score 366; DB 7;
93.9%; Pred. No. 5.8e-38;
iive 3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB61810 standard; protein; 66 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2001; 2001US-0332300P. 08-APR-2002; 2002US-0370934P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66 AA;
          domain.
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WPI; 2003-513532/48.
                                                                                                                                                                                                                                                                                                                            Similarity
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Matches
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17-JUN-2004

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The invention comprises a method for providing a labelled target protein/peptide. The method involves contacting a chemical compound with affinity support, removing impurities in the reaction mixture surrounding the affinity support to which the chemical molecule is bound, and cleaving or eluting the molecule from the affinity support to obtain irreversible or reversible affinity tagging residue, labelled target protein or labelled peptide. The method of the invention is useful for labelling a target protein/peptide or high throughput screening assay. The method of the invention is useful for identifying agents that modulate the activity or characteristics of a target protein/peptide such agents are useful as pharmaceuticals. The present amino acid sequence represents the BIR-3 domain from the human XIAP protein which was used in an example of the invention.
                                                                                                                                               Providing labeled target protein or target peptide by contacting chemical compound with affinity support, removing impurities in reaction mixture surrounding affinity support, cleaving or eluting chemical molecule from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitor of apoptosis protein; IAP; testis; TIAP; apoptosis; inhibitor; fertility; testicular cancer; male infertility; male birth control; X-linked inhibitor of apoptosis protein; XIAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.8%; Score 366; DB 8; Length 11
95.5%; Pred. No. 1.1e-37;
ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG32418 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                Example 6; Page 46; 81pp; English.
                                                   Seifert J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification"
(NOVS ) NOVARTIS PHARMA GMBH
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99US-00239867
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                                             Auer M, Meisner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KORN/) KORNELUK R G.
                                                                                                 WPI; 2004-480677/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                affinity support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 110 AA;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a substantially pure polypeptide having a charles that loo amino acids and capable of forming a complex with a polypeptide that includes a baculovirus inhibitor of apoptosis repeat (BIR) domain. The apoptosis pathway is known to play a critical role in embryonic development, viral pathogenesis, cancer, autoimmune disorders and neurodegenerative diseases. The failure of the apoptocit response has been implicated in the development of cancer, autoimmune disorders communed in the development of cancer, autoimmune disorders of en implicated in the development of cancer, autoimmune disorders of cample systemic lupus erythematosis and multiple sclerosis) and viral infections (including herpes virus, poxvirus and adenovirus. The infections (including herpes virus, poxvirus and adenovirus. The cample systemic lapped to the form the main lapped to the proteases (BIR) domains. Human LAPS, XIAP, HIAPI (CIAP2) and HIAP2 (CIAP4) all posses three BIR domains and carboxy terminal RING zinc fingers. The lappe bind and inhibit caspases -3, -7 and which inhibit the activity of IAPS may therefore have extostatic activity through the enhancement of apoptosis. The polypeptides of the invention of are candidate peptide ligands for binding to the BIR domain of IAPS. They are candidate peptide ligands for binding to the BIR domain of IAPS. They are leaveful for the treatment of cancer and other neoplasms, such as an entition and proposal and the propertions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemias, colon carcinoma, cervical cancer, uterine cancer, testicular cancer, small cell lung carcinoma, uterine cancer, renal cell carcinoma and Wilm's tumour, and for enhancing apoptosis. The present sequence is that of the human inhibitor of apoptosis (IAP) protein XIAP BIR3 domain against which the peptides of the invention are targeted to bind.
                          Polypeptide capable of forming a complex with a polypeptide comprising a baculovirus inhibitor of apoptosis repeat domain useful for treating
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Pred. No. 5.8e-38;
1; Mismatches 2; Indels
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                                                                                                                                    Disclosure; Fig 1A; 53pp; English.
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95.5%;
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                                                                                   cancer and other neoplasms.
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                                                                                                                                    A substantially pure TIAP polypeptide (I), a member of IAP (inhibitor of apoptosis) family of proteins that is expressed in the testes. (I) is useful for identifying a compound that modulates TIAP biological activity (I) is useful for increasing apoptosis in a cell, preferably a germ-line cell and for increasing apoptosis which occurs as a part of testicular treating or preventing apoptosis which occurs as a part of testicular cancer and male infertility. TIAP may be manipulated for use as a male birth control. TIAP polypeptides and nucleic acid sequences also have diagnostic use in the detection or monitoring of conditions involving aberrant levels of apoptosis. The present sequence represents the amino acid sequence of X-linked inhibitor of apoptosis protein, XIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                Novel polypeptide, a member of inhibitor of apoptosis family of proteins that is expressed in testes useful for modulating apoptosis in cells, particular cells involved in male fertility.
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95.5%; Pred. No. 2.6e-37;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein of APP related human homologue hCP35211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO20511 standard; protein; 278 AA.
                                                                                                                     Example 3; Fig 4B; 24pp; English
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14-JUN-2001; 2001US-0298309P.
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Best Local Similarity 95.5
Matches 63; Conservative
                       Σ
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                       Korneluk RG, Lagace
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N-PSDB; AAK99405.
                                            WPI; 2002-642245/69.
                                                                                                                                                                                                                                                                                                                                                                                61 PGCKYL 66
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   LAGACE M.
                                                         N-PSDB; ABS52803
                                                                                                                                                                                                                                                                        Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200226820-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA020511;
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   (LAGA/)
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The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid conding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence concodes a 123 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-concoder control sequence. Expression of the sequence gives the fip an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligomucleotide, double constrained RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheinmer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This sequence represents the protein of the APP related human homologue hCP35211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 YEARIFTFGTWIYSYNKEQIARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis inhibitor, X-linked inhibitor of apoptosis protein, XIAP; HIV; AIDS; neurodegeneration, myelodysplastic syndrome, ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY
New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 366; DB 5; Length 21:e
Pred. No. 3.1e-37;
Pred. No. 3.2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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/label= Ring_zinc_finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                         Example 4; Page 112; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW19581 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human apoptosis inhibitor XIAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6. .93
|abel= BIR-1
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/label= BIR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265. .330
/label= BIR-3
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95US-00576956.
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95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 95.5
nes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGCKYL 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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Matches
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(UYOT-) UNIV OTTAWA

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Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; XIAP protein.
                                                                                                                                                                                                                                                           AAW69294 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                          97US-00800929
                                                                                                                                                                                                                                                                                                                                                               98WO-IB000781
                                                                                                                                                                                                                                                                                                                                                                                                   AE,
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Mackenzie
                       WPI; 1997-154262/14
                                                                                                                                                                                                                            PGCKYL 330
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-467164/40.
N-PSDB; AAV55038.
                                                                                                                                                                                                                                                                                                                                                                                      (UYOT-) UNIV OTTAWA
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                  61 PGCKYL 66
                                                                                                                                                                                                                                                                                             Human XIAP protein
                            N-PSDB; AAT70836.
                                                                                                                                                        Sequence 497 AA;
           Korneluk RG,
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                      WO9835693-A2
                                                                                                                                                                                                                                                                                                                                                               13-FEB-1998;
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                                                                                                                                                                                                                                                                                  13-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                  Korneluk R,
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                       AAW69294;
                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                               RESULT 12
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This sequence is the human XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits of proliferative disease, specially cancers of compounds are used to treat proliferative diseases, specially cancers of compounds are used to treat proliferative diseases, specially cancers of covary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyroid, central nervous system, prostate, colon, cettum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, consistent and are associated with poor prognosis, suggested that wild-type p53 suppresses transcription of the IAP or NAIP censes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors
specifically applied to cancers involving p53 mutations.
                                                          Disclosure, Fig 1, 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 497 AA;
and NAIP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                              Human XIAP, HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2 (AAM19581-86) are a new class of mammalian proteins that are inhibitors of apoptosis (IAP) and which are characterised by the presence of a ring zinc finger domain (see also AAW19587) and at least one BIR (baculovirus IAP repeat) domain (see also AAW19589). The XIAP amino acid sequence was deduced from the xiap gene (AAT70836) isolated from a human foetal brain or in vivo) and used in methods can be expressed in host cells (in vitro or in vivo) and used in methods for treating diseases and disorders having apoptosis, sep. in a human diagnosed as HIV-positive or as having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or reperfusion injury, or a toxin-induced liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 YEARIFITEGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWEQHAKWY 324
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                                                                                                                                                                                             Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 366; DB 2; Length 497; 95.5%; Pred. No. 6.1e-37; Live 1; Mismatches 2; Indels
                                                    Liston P;
                                                 Baird S,
                                                                                                                                                                                                                                                                                                                      Claim 27; Page 68-70; 219pp; English.
                                             Mackenzie AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Conservative
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0
                                                             Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta.
                                               1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein.
                            ö
  Length 497;
94.8%; Score 366; DB 2; Length 49
95.5%; Pred. No. 6.18-37;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 28-30; 43pp; Japanese.
                                                                                                                                                                                 AAY59451 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-00130378
                                                                                                                                                                                                                                                                                                                                                                                                                                 98JP-00130378
                                                                                                                                                                                                                                                        Human XIAP protein sequence
                                                                                                                                                                                                                                 (first entry)
          l Similarity 95.5
63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MATS/) MATSUMOTO K.
                                                                                                                     325 PĠĊKYĽ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-078337/07.
                                                                                              PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ48862
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              JP11326328-A
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                                                                                                                                                                                                                                 24-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-1999
                                                                                                                                                                                                         AAY59451;
                                                                                                                                                         RESULT 13
                                                                                                                                                                       AAY59451
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This sequence represents the human XIAP protein. The invention relates to a method for screening a substance inhibiting the formation of a complex

Inducing apoptosis in proliferative mammalian cells with inhibitor of or NAIP polypeptide - also methods for prognosis based on presence of

Pratt

ä Tsang

Baird S,

Liston P,

Length 497;

Sequence 497 AA;

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            (XIAP), transforming growth factor-beta activated kinase I(TAKI) binding protein 1(TABI) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TABI is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TABI and XIAP as well as between XIAP and TGF-beta (Transforming growth factor-beta) type I and/or type II receptor is useful as a drug
between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein
                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                Score 366; DB 3; Length 497;
Pred. No. 6.1e-37;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          94.8%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
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                                                                                                                                                                                                                                                                                            Sequence 497 AA;
                                                                                                                                                                                                                                                                                                                                          Query Match
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265 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY 324 9 1 YEARIVIFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 325 PGCKYL 330 99 PGCKYL 61 qq ਨੇ Š

X-linked inhibitor of apoptosis; XIAP; hLLP; MIHA; U45880; antisense; antiinflammatory; cytostatic; tumour. Human X-linked inhibitor of apoptosis. AAY99985 standard; protein; 497 AA (first entry) AAY99985 RESULT 14 AAY99985 

99US-00392580. Homo sapiens 09-SEP-1999; US6087173-A. 11-JUL-2000

Ackermann EJ; Cowsert LM, WPI; 2000-498201/44. Bennett CF,

99US-00392580

09-SEP-1999;

(ISIS-) ISIS PHARM INC

N-PSDB; AAA64901.

The present invention relates to antisense oligonucleotides designed to inhibit expression of the human X-linked inhibitor of apoptosis (the present sequence). Modified phosphorothioace 2-MOS oligonucleotides are more effective inhibitors than unmodified oligonucleotides. The oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis expression in cells and tissues in vitro. The oligonucleotides are also useful for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to prevent infection, inflammation or tumour formation Antisense compound useful for research reagents, diagnostics, prophylaxis and for treating disorders associated with X-linked inhibitor of apoptosis, modulates expression of X-linked inhibitor of apoptosis. Example 13; Col 43-48; 33pp; English

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The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPL or HIAPP. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of composition comprising a mammalian IAP antisense molecule and a method of antisense inhibitor is useful for channing apoptosis in a cell. The IAP antisense inhibitor is useful for channing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer.) adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                           265 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative
                                                                      09
                                                                      1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                                       Gaps
                                     ..
                                     Indels
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Score 366; DB 3; L
Pred. No. 6.1e-37;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                 Human inhibitor of apoptosis, XIAP.
                                                                                                                                                                                                                                                                                     ABG65663 standard; protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Fig 1; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AEGE-) AEGERA THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001; 2001WO-CA001379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000; 2000US-00672717.
   94.8%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                            26-AUG-2002 (first entry)
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lacasse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-479562/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UYOT-) UNIV OTTAWA
                                                                                                                                                                                         325 PGCKYL 330
                       Local Similarity
                                                                                                                                                      61 PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK93869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                         63;
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   Query Match
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protein sequence SX SS

Sequence 497 AA;

Query Match 94.8%; Score 366; DB 5; Length 497; Best Local Similarity 95.5%; Pred. No. 6.1e-37; Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps

· 0

61 PGCKYL 66 |||||| 325 PGCKYL 330

9y 0b

95 PP 95

Search completed: October 22, 2004, 11:16:32 Job time : 116.284 secs

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GenCore version 5.1.6
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October 22, 2004, 10:50:26; Search time 125.104 Seconds (without alignments) 303.544 Million cell updates/sec Run on:

US-09-654-743-24

Title: Perfect score:

386 1 YEARIVTFGTWIYSVNKEQL......KPSEDPWDQHAKCYPGCKYL BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1825181 seqs, 575374646 residues Searched:

1825181

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

SUMMARIES	Description	AT	OgesfO rattus	JMAN P98170 homo sa	40peq0	OSEG05 rattus	MOUSE 060989 mus mus	JMAN 09600 homo	Ofpia0 homo	18 Aah39318 hon	omod Ivaigo		PANTR 095m72 pan tro	GORGO 095m71	O96rW6 homo sar	OSUVEB GRAIT	4 O8wmv4 bos tal	O6dbv7 brac	OBIIWho	076811	Oévtv9	88 Aad9168	BIR3 HUMAN 013489 homo sapien		1G 062640	09ia70 gall	201969 9allus	Ogese of rattus	IICK 090660 gallus	PVOP P41437 ordvia	Official Agrotis	arao tan a funcia
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### ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA.";
Submitted (OCT-1999) to the BMBL/GenBank/DDBJ databases.
-!- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1-SUBUNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).
-1-SUBCELLUAR LOCATION: Cytoplasmic (By similarity).
-1-DOMAIN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition.
The interactions with SMAC and PRSS25 are mediated by the second and third BIR domains (By similarity).
-1-SIMILARITY: Belongs to the IAP family.
-1-SIMILARITY: Contains 3 BIR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Baculoviral IAP repat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked inhibitor of apoptosis protein) (X-linked inhibitor of apoptosis protein) (X-linked Inhibitor of apoptosis protein) (X-linked IAP)
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InterPor; IPR001370; BIR.
InterPor; IPR001841; Znf_xing.
Pfam; PF00653; BIR; 3.
SWART; SW00238; BIR; 3.
SWART; SW00184; RING; 1.
PROSITE; PS01282; BIR REPEAT_1; 3.
PROSITE; PS01282; BIR REPEAT_2; 3.
PROSITE; PS00518; ZF_RING_1; PALSE_NEG. PROSITE; PS00918; ZF_RING_2; 1.
PROSITE; PS00981; ZF_RING_2; 1.
PROSITE; PS00981; ZF_RING_2; 1.
PROSITE; PS00981; ZF_RING_2; 1.
REPEAT_26691; REPEAT_26781.
REPEAT_26691; REPEAT_26781.
REPEAT_26691; REPEAT_26781.
REPEAT_26691; REPEAT_26781.
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                                                                                 STANDARD;
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Q9R016;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holcik M., Lefebyre C.A., Hicks K., Korneluk R.G.,
"Cloning and characterization of the rat homologues of the Inhibitor
of Apoptosis protein 1, 2, and 3 genes.";
BMC Genomics 3:5-5(2002).
EMBL, AR183429; AAG22969.1; -.
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E250E3C77461A469 CRC64;
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Last annotation update)
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Pred. No. 4.4e-35;
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PROSITE; PSSO143; BIR REPEAT 2; 3.
PROSITE; PSSO1089; ZF RING 2; 11.
SEQUENCE 496 AA, 56117 MM; 9BE
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                                                   56072 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Gilfillan M.C., Shiels H., Hardwick J.M., Thompson C.B.;
"A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors.";
EMBO J. 15:2685-2694(1996).
01-OCT-2004 (Rel. 45, Last annotation update)
Baculoviral IAP repeat-containing protein 4 (Inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
                                                                                                                                                                                                                                                                                                                                          MEDLINE=96149249; PubMed=8552191;
Liston P., Roy N., Tamai K., Lefebyre C., Baird S., Cherton-Horvat
Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
"Suppression of apoptosis in mammalian cells by NAIP and a related
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Deveraux Q.L., Takahabhi R., Salvesen G.S., Reed J.C.;
"X-linked IAP is a direct inhibitor of cell-death proteases.";
Nature 388:300-304(1997).
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MEDLINE=21020961; PubMed=11140637; DOI=10.1038/35050006;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                 Name=BIRC4; Synonyms=API3, IAP3, XIAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal heart;
MEDLINE=96256286; PubMed=8654366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         family of IAP genes.";
Nature 379:349-353(1996).
                                                                                       (IAP-like protein) (HILP)
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BIR 2.
BIR 3.
RING-type.
D->S: Reduced interaction with PRSS25.
E->S: Decreased interaction with SWAC and with PRSS25.
S -> C (in Ref. 1).
Q -> P (in Ref. 2).
                                                                                    -i- FUNCTION: Apoptotic suppressor. Inhibitor of caspase-3, -7 and -9-1- SUBGNIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- TISSUE SPECIFICITY: Ubiquitous, except peripheral blood
                                                                                                                                                                                         -!- DOWALN: The second BIR domain is sufficient to inhibit caspase-3 and -7, while the third BIR is involved in caspase-9 inhibition. The interactions with SWAC and PRSS25 are mediated by the second and third BIR domains.
-!- SIMILARITY: Belongs to the IAP family.
-!- SIMILARITY: Contains 3 BIR repeats.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
Liu Z., Sun C., Olejniczak E.T., Meadows R.P., Betz S.F., Oost T., Herrmann J., Wu J.C., Fesik S.W., "Structural basis for binding of Smac/DIABLO to the XIAP BIR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              # PDB; 1C90; NMR; A=124-240.

# PDB; 1C90; NMR; A=237-356.

# PDB; 1C90; NMR; A=237-356.

# PDB; 1G91; NMR; A=240-240.

# PDB; 1G95; NMR; A=240-240.

# PDB; 1130; X-ray; E/F=120-240.

# PDB; 1130; X-ray; E/F=124-240.

# PDB; 1130; X-ray; C/D=124-242.

# PDB; 1151; X-ray; C/D=124-242.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=124-240.

# PDB; 1NM9; X-ray; C/D=120-240.

# PDB; 1NM; A=200-240.

# PDB; 1NM; A=200-240.

# DB; 1NM; A=200-240.

# DB; 1NM; A=200-240.

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EMBL, U32974; AAC50518.1; --
EMBL, AL121601; CAB95312.1; --
EMBL, BC032729; AAH32729.1; --
PIR; S69544; S69544.
                                                                       Nature 408:1004-1008(2000).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Regulated expression of inhibitor of apoptosis protein 3 in the rat corpus luteum.";
Biol. Reprod. 68:2232-2240(2003).
BMB1. AF304334; AAG41193.1; -.
BMB1. AF304334; AAG41193.1; -.
GO, GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
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MEDLINE=22642584; PubMed=12606402;
Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Friis R.R.,
Dharmarajan A.M.;
                                                                                                                                                                                                                                                                                                                                                                Length 497;
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95.5%; Pred. No. 4.4e-35;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        56684 MW; 9D394C16D45EB635 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Inhibitor of apoptosis protein 3.
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325
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343
497 AA;
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Best Local Similarity
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324 PGCKYL 329
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Regulated expression of inhibitor of apoptosis protein 3 in the
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MEDLINE=22642584; PubMed=12606402;
Lareu R.R., Lacher M.D., Bradley C.K., Sridaran R., Friis R.R.,
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R HSSP; P98170; II51.

R GO; GO:000151; C:ubiquitin ligase complex; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0006916; P:anti-apoptosis; IEA.

R GO; GO:0006916; P:anti-apoptosis; IEA.

R GO; GO:001687; P:procein ubiquitination; IEA.

R InterPro; IPR001370; BIR.

DR FAMAR; SM00238; BIR; 3.

DR SMARY; SM00238; BIR; 3.

DR ROSITE; PS01282; BIR; 3.

DR ROSITE; PS50189; BIR REPEAT_1; 3.

DR ROSITE; PS50189; ZF RING 2; 1.

SEQUENCE 501 AA; 56548 MW; 0973FBF28EBIC5A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          Length 501;
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01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Inhibitor of apoptosis protein 3.
                               GO, GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; Pro6653; BIR; 3.
SMART; SM00238; BIR; 3.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR REPEAT_1; 3.
PROSITE; PS50143; BIR REPEAT_2; 3.
PROSITE; PS50143; BIR REPEAT_2; 3.
PROSITE; PS50089; ZF RING, 2; 1.
SEQUENCE 501 AA; 56578 WW; 4863F69FF2E0CGCD C
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            GO:0006916; P:anti-apoptosis; IEA
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bloj. Reprod. 68:2332-2240(2003).
EMBL; AF304333; AAG41192.1; -.
HSSP; P98170; 1151.
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HSSP;
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(29670); Ogerws;
28-FEB-2003 (Rel. 41, Created)
05-UL-2004 (Rel. 44, Last sequence update)
05-UL-2004 (Rel. 144, Last annotation update)
Bacultoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-inhibitor of apoptosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M MEDLINE=1286921; PubMed=11390657;

M MEDLINE=21286921: PubMed=11390657;

N DOI=10.1128/MCB.21.13.4292-4301.2001;

R Richter B.W.M., Mir S.S., Elben L.J., Lewis J., Reffey S.B.,

R Rattinia A., Tian L., Frank S., Youle R.J., Nelson D.L.,

A Notarangelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.,

"Molecular cloning of ILP-2, a novel member of the inhibitor of
apoptosis protein family";

Mol. Cell. Biol. 21:4292-4301(2001).

- FUNCTION: Protects against apoptosis mediated by BAX.

-! SUBCELULAR LOCATION: Cytoplasmic (Probable).

-! SUBCELULAR LOCATION: Cytoplasmic (Probable).

-! SUBCILULAR LOCATION: Cytoplasmic (Probable).

-! SUBLIARITY: Belongs to the IAP family.

-! SIMILARITY: Contains 1 BIR repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=21481900; PubMed=11597143; DOI=10.1006/geno.2001.6635;
Lagace M., Xuan J.-Y., Young S.S., McRoberts C., Maier J.,
Rajcan-Saparovic B., Korneluk R.G.,
"Genomic organization of the X-linked inhibitor of apoptosis and identification of a novel testis-specific transcript.";
Genomics 77:181-188(2001).
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322 W -> C (in Ref. 2).
346 S -> P (in Ref. 2).
360 S -> P (in Ref. 2).
449 C -> S (in Ref. 2).
462 V -> P (in Ref. 2).
468 V -> P (in Ref. 2).
490 K -> N (in Ref. 2).
56079 MW; ECSFAE0799F2CDDB CRC64;
                                                                                                                                                                                                                                                                                             5.3e-34;
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Pred. No. 5.3e-34;
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1 Similarity 93.9%;
62; Conservative
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                                                                                                                                                                                                             496 AA;
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A Klausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McWann P.J., Wockernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Giabs R.A.,

Rahe J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Youchman J.W., Green B.D., Dickson M.C.,

Rak Rizzyunski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rand Rayseley R. M., Nan M., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 1.4e-31;
8; Mismatches 4; Indels
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RING-type.
Y -> H (in Ref. 2).
; CB7F034B0DDFAD9D CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                           HSSP, P98170; 1G73.
Genew; HGNC:14878; BIRC8.
InterPro; IPRO01370; BIR.
InterPro; IPRO01370; BIR.
InterPro; IPRO01370; BIR.
SMART; SMO0238; BIR; 1.
SMART; SMO0184; RIR; 1.
PROSITE; PSO1282; BIR REPEAT 1; 1.
PROSITE; PSO50143; BIR REPEAT 2; 1.
PROSITE; PSO5018; ZF_RING_1; FALSE_NEG.
PROSITE; PSS50089; ZF_RING_2; 1.
APODICSi8; Zinc-finger.
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EMBL; AF420440; AAL30369.1;
EMBL; AF164682; AAK81892.1;
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TISSUE=Testis;
Strausberg R.;
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Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Attschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toofhiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Widnin T.B., Toofhiyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Wokin T.B., Toofhiyuki S., Carninci P., Wullahy S.J.,

R. Basak S.A., McKwan D.J., McKernan R.J., Marke J.A., Gunarane P.H.,

R. A. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R. Halton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Riching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Richinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human

R. Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                               EMBL, BC039318; AAH39318.1; -.
InterPro; IPR001841; Znf_ring.
Ffam; PF00653; BIR; 1.
SMART; SM00238; BIR; 1.
SMART; SM00348; RIR; 1.
PROSITE; PS01282; BIR_REPEAT_1; 1.
PROSITE; PS00193; BIR_REPEAT_2; 1.
PROSITE; PS0089; ZFRING_2; 1.
SEQUENCE 236 AA; Z7077 WW; DF38350311FDAFBF CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                          86.5%; Score 334; DB 2;
81.8%; Pred. No. 1.4e-31;
ive 8; Mismatches 4;
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MEDLINE=22388257; PubMed=12477932;
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(TrEMBLrel. 27, I
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ses 54; Conservative
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14-APR-2004
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EMBL; BC03
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MEDINE-2238257; Pubmed=12477932;

MEDINE-2238257; Pubmed=12477932;

MEDINE-2238257; Pubmed=12477932;

MEDINE-2238257; Pubmed=12477932;

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antachenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Porshyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Raha S.A., McIny D.M., Soderia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Soderian B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Soderian A.M., Gay L.J., Hulyk S.W.,

Rahakesley R.W., Touchman W., Madan A., Rodrigues S., Sanchez A.,

Blakesley R.W., Touchman W., Schen E.D., Dickson M.C.,

Blakesley R.W., Touchman W., Schen E.D., Dickson M.C.,

Antiquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Krzywinski M.L., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;
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4 YEARLITFGTWMYSVNKEQLARAGFYAIGQEDKVQCFHCGGGLANWKFKEDPWEQHAKWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-BÎRC8;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;

L. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R. MicrFro; IPRO01370; BIR.

R. InterPro; IPRO01341; Znf_ring.

R. InterPro; IPRO0141; Znf_ring.

R. SMART; SM00238; BIR; 2.

R. SMART; SM00184; RIR; 2.

R. SMART; SM00184; RIR; 2.

R. SMART; SM00184; RIR; 2.

R. SMART; SM00184; RIR; 2.

R. PROSITE; PS01282: BIR REPEAT 1; 2.

DR. PROSITE; PS0143; BIR_REPEAT 2; 2.

DR. PROSITE; PS50143; BIR_REPEAT 2; 2.

DR. PROSITE; PS50189; ZR RING 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                       338 AA
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Best Local Similarity
Matches 54; Conserv
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SEQUENCE FROM N.A.
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RX Strauber from N.A.

RX Strauberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,

RA Strauberg R.L., Fedingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Arapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Moremson R.D., Mullahy S.J.,

RA Brownstein W.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R. Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. J. Marra M.A.;

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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last amnotation update)
Baculoviral IAP repeat-containing protein 8 (Inhibitor of apoptosis-like protein 2) (IAP-like protein 2) (ILP-2).
Name-BIRC8; Synonyms-ILP2;
Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.5%; Score 334; DB 2; Length 338; 81.8%; Pred. No. 2e-31; live 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071665; AAH71665.1; -.
SEQUENCE 338 AA; 38622 MW; DC17979CFC92E4DF CRC64;
                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                      338 AA
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                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
      166 PGCKYL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           BIRC8 protein.
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Q95M72;
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ACCOMMENT OF THE COMMENT OF
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
05-ULL-2004 (Rel. 44, Last annotation update)
16-ULL-2004 (Rel. 47, Last annotation update)
11-2004 (Rel. 47, Last annotation update)
11-2004 (Rel. 47, Last annotation update)
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11-2004 (Rel. 41, Last sequence)
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11-2004 (Rel. 41, Last sequence)
11-2004 (Rel. 41, Last sequence)
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                                                                                                                                         MEDLINE=2128691; PubMed=11390657;
DOI=10.1128/MCB.21.11.4292-4301.2001;
Richter B.W.M., Mir S.S., Eiben L.J., Lewis J., Reffey S.B.,
Frattini A., Tian L., Frank S., Youle R.J., Nelson D.L.,
Notarnagelo L.D., Vezzoni P., Fearnhead H.O., Duckett C.S.,
Wolecular cloning of ILP-2, a novel member of the inhibitor of
apoptosis protein family ".
Mol. Cell. Biol. 21:4292-4301(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64CCA3A251420EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: Belongs to the IAP family.
-i- SIMILARITY: Contains 1 BIR repeat.
-i- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Binds to caspase-9 (By similarity)
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InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_ring.
Pfam; Pr00653; BIR; 1.
SMART; SM00184; RIR; 1.
SMART; SM00184; RING; 1.
PR05ITE; PS01282; BIR_REPEAT_1; 1.
PR05ITE; PS01218; BIR_REPEAT_2; 1.
PR05ITE; PS00518; ZF_RING_1; FALSE_NEG.
Apptcs18; Znc-finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY030052; AAK49776.1; -.
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                                                                                                                 SEQUENCE FROM N.A.
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                                        NCBI_TaxID=9598;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                    DOI=10.1128/MCB.21.13.4292-4301.2001, Edwis J., Reffey S.B., Richter B.W.M. Mir S.S., Eiben L.J., Lewis J., Reffey S.B., Frattinia A., Tian L., Parattinia R., Tian L., Vaule R.J., Nelson D.L., Notarangelo L.D., Vazzoni P., Fearnhead H.O., Duckett C.S., "Molecular cloning of ILP-2, a novel member of the inhibitor of apoptosis protein family.", Mol. Cell. Biol. 21.4292-4301(2001).

-: FUNCTION: Protects against apoptosis mediated by BAX (By
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Mir S.S., Duckett C.S.;

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, P8164061, AAK81891.1; -.

HSSP, P98170; 163F.

GO; GO:0005622; C:intracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 RING-type.
27120 MW; C3A70E39EE442E4C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                           similarity).
--- SUBUNIT: Binds to caspase-9 (By similarity).
--- SUBCELLUIAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the IAP family.
--- SIMILARITY: Contains 1 BIR repeat.
--- SIMILARITY: Contains 1 RING-type zinc finger.
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INTERPOS INTROUBALI, SELVING.

INTERPOS INTROUBALI, SELVING.

PERM, PRO0653; BIR; 1.

SMART; SM00184; RIR; 1.

SMART; SM0184; RING; 1.

PROSITE; PS01282; BIR REPEAT 1; FALSE_NEG.

PROSITE; PS00184; ZF_RING 1.

PROSITE; PS00184; ZF_RING 2; T.

PROSITE; PS00184; ZF_RING 2; 1.
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          MEDLINE=21286921; PubMed=11390657;
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236 AA;
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Bukaryota metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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Bridgham J.T., Johnson A.L.;

Bridgham J.T., Johnson A.L.;

Bridgham J.T., Johnson A.L.;

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-:-SIMILANITY: Contains 1 RING-type zinc finger.

EMBL; A4451854; A247170.1; -.

R GO; GO:0000151; C:ubiquitin ligase complex; IEA.

GO; GO:00008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0006916; P:anti-apoptosis; IEA.

GO; GO:0006916; P:anti-apoptosis; IEA.

R InterPro; IPR001841; Znf_ring.

R InterPro; IPR001841; Znf_ring.

P Ffam; PP00067; BIR; 3.

R PROSITE; PS01283; BIR; 3.

R PROSITE; PS01284; BIR REPEAT 1; 2.

R PROSITE; PS01284; BIR REPEAT 2; 3.

R PROSITE; PS01284; BIR REPEAT 2; 3.

R PROSITE; PS01284; BIR REPEAT 2; 3.

R PROSITE; PS01283; BIR ZERNG-finger.

O SEQUENCE 493 AA; 55251 MW; 030A9F56CB6119BC CRC64;
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                                                                                                                                                                                79.3%; Score 306; DB 2; Length 106; 91.1%; Pred. No. 1.3e-28; Indels iive 3; Mismatches 2; Indels
                                                                                                                                    6BBAD3AEA880A891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Inhibitor of apoptosis protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 AA
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GO, GO:0006916; P:anti-apoptosis; IEA. InterPro; IPR01170; BIR. Pfam; PR00653; BIR; 1. SMART; SM00238; BIR; 1. PROSITE; PS50143; BIR REPEAT 2; 1. SEQUENCE 106 AA; 12360 MW; 6BBAD3A
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                                                                                                                                                             Query Match
Best Local Similarity 91.1..
Thes 51; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 22, 2004, 11:08:02; Search time 23.1493 Seconds (without alignments) 274.320 Million cell updates/sec

US-09-654-743-24 386 1 YEARIVTFGTWIYSVNKEQL......KPSEDPWDQHAKCYPGCKYL 66 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0.
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Description	apoptosis inhibito apoptosis inhibito apoptosis inhibito inhibitor of apoptosis inhibito apoptosis inhibito apoptosis-inhibiti apoptosis-inhibito kidney inhibitor o inhibitor-of-apoptosis inhibito apoptosis inhibito apoptosis inhibito probable apoptosis inhibito probable apoptosis inhibito probable apoptosis inhibito apoptosis inhibito off.13 protein - Au IAPI orf.3 protein - Au IAPI orf.3 protein - Ei ORF MSV242 probable apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis apoptosis inhibito apoptosis apoptosis inhibito apoptosis apoptosis inhibito apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apoptosis apo	
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Score	1986 1986 1986 1986 1986 1987 1987 1988 1988 1988 1988 1988 1988	
Result No.	111111111111111111111111111111111111111	

apoptosis inhibitor hiap-1 - human C;Species: Homo sapiens (man) C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004 C;Accession: S68449 R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,

RESULT 2 S68449

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65	64.5	64.5	7	40	63	62.5	61.5	61.5	60.5	60.5	60.5	9	9	9	59.5	59.5
30	31	32		n :	4	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT S69544 apoptos	RESULT 1 869544 apoptosis inhibitor IAP homolog - human
C;Speci C;Date: C;Acces	C.Species: Homo sapiens (man) 
 R; Ducker EMBO J.	R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C EMBO J. 15, 2685-2694, 1996
A;Title A;Refere A;Access	A,Title: A conserved family of cellular genes related to the baculovirus iap gene and en. **Reference number: 869544; MUID:96256286; PMID:8654166 A;Accession: 86944
A;Statum A;Molecu	A;Status: preliminary; nucleic acid sequence not shown A;Molecule rype: mkWA b:Decid:Acon and
A; Cross- R; Listor	A. Cross-references: UNIPROT: P98170; EMBL: U32974; NID: 91016687; PIDN: AAC50518.1; PID: 9101. R. Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
A; Title: A; Refere	nacture 3/3, 3497-333, 1996 Affittle: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP AfReference number: A58182; MUID:96149249; PMID:8552191
A; Access A; Status	A,Accession: S68451 A,Status: nucleic acid sequence not shown
A; Molecule A; Residues: A; Cross-ref C:Genetics:	A;Molecule type: mRNA A;Residues: 1-161, C',163-422, Q',424-497 <lis> A;Croserences: EMBL:U45880; NID:g1184319; PIDN:AAC50373.1; PID:g1184320 C:Genetics:</lis>
A, Gene: ilp C, Function:	ilp on:
A;Descri C;Superf C;Keywor F;446-49	A,Description: apoptotic suppressor C,Superfamily: apoptosis inhibitor IAP homolog; RING finger homology C,Keywords: apoptosis; zinc finger F;446-490/Domain: RING finger homology <rrn></rrn>
Query Match Best Local Matches 6	Ouery Match  94.8%; Score 366, DB 2; Length 497;  Best Local Similarity 95.5%; Pred. No. 2e-33;  Matches 63; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
δ	1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKFSEDPWDQHAKCY 60
qa	265 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY 324
ò	61 PGCKYL 66
qa	325 PGCKYL 330

9

5;

Length 268;

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apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis viru C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004 R;Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyp
A;Reference number: A53989; MUID:94187094; PMID:8139034
A;Accession: A53989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P41437, GB:L22564, NID:9456111, PIDN:AAB02610.1, PID:9456114
A,Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As C,Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YEARIVIFGTWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: S68450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ARIVIFGIWIYSVNK--EQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY
                                                                                                                           3 ARIVTFGTWIYSVNK--EQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.2%; Score 190; DB 2; Length 268; 48.5%; Pred. No. 6.7e-14; Live 12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 184; DB 2; Length 61
Pred. No. 7e-13;
9; Mismatches 22; Indels
            49.2%; Score 190; DB 2;
48.5%; Pred. No. 6.7e-14;
iive 12; Mismatches 20;
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C;Keywords: apoptosis; zinc finger
F;567-611/Domain: RING finger homology <RNG>
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A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis inhibitor hiap-2 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.5%;
watches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 48.5%
Matches 32; Conservative
                  Query Match
Best Local Similarity 48.5%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                            |:|:
173 DRCEYV 178
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A;Residues: 1-618 <LIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-268 <BIR>
                                                                                                                                                                                                                                                          61 PGCKYL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 868450
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A; Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A; Reference number: Z17011; MUID: 97271300; PMID: 9126251
A; A,Accession: T10304
A; A,Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule Type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cross-references: UNIPROT:062640; GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g29571; 351/Domain: RING finger homology <RRN>
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAF
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAF
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: 868449
A;Accession: 868449
A;Andlecule type: mRNA
A;Nolecule type: mRNA
A;Cross-references: UNIPROT:Q13489; EMEL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g118
C;Function:
C;Function:
C;Keywords: apoptosis; zinc finger
F;553-597/Domain: RING finger homology <RNG>
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Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: O4-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
Cipate: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
Cipate: 05-Session: JC5964 Martin, R.; Binder, B.R.; Lipp, J.
Biochem Biophys. Res. Commun. 243, 827-832, 1998
Ajfitle: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap)
Aireference number: JC5964; MuID:98162622; PMID:9501011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Orgyia pseudotsugata nuclear polyhedrosis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YEARIVIFGIWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAK 58
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A, Cross-references: EMBL: U75930; NID: 92934903; PIDN: AAC59034.1; PID: 91911281
C; Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F; 217-261/Domain: RING finger homology <RRN>
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C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YEARIVIFGIWIYS--VNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAK
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                                                                                                                                                                                                                                                                                                                                                                                51.3%; Score 198; DB 2; Length 60
55.9%; Pred. No. 1.8e-14;
iive 6; Mismatches 22; Indels
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150 WFPRCEYL 157
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315 WFPRCEYL 322
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A;Molecule type: DNA
A;Residues: 1-358 <STE>
A;Cross-references: UNIPF;307-351/Domain: RING fil
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Best Local Similarity
Matches 38; Conserv
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Gaps 5; 1;

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Length 618;

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C,Accession: A55478
R;Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird, & J. T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A.
A;Tille: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi A;Accession: A55478
MUDD:95112344; PMID:7813013
A;Molecule type: mRNA
A;Kesidues: 1-1232 cROY>
A;Kesidues: 1-1232 cROY>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:SMA@; SWA
A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A;Map position: 5q12.2-5q13
C;Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot F;94-110/Domain: transmembrane #status predicted <TWM1>
F;470-477/Region: nucleotide-binding motif A (P-loop)
F;479-496/Domain: transmembrane #status predicted <TWM2>
F;476/Binding site: ATP (Lys) #status predicted
F;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuronal apoptosis inhibitory protein 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42628
R;Yarashi, Z; Diez, E; Gros, P.; MacKenzie, A.
Mamm. Genome 10, 761-763, 1999
A;Title: CDNA cloning and the 5'genomic organization of Naip2, a candidate gene for muri:
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A;Cross-references: UNIPROT:09QUK4; EMBL:AF102871; NID:93860228; PID:93860229; PIDN:AAC7:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                    C;Species: Homo sapiens (man)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 BARIVTFGTW---IYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAK
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41.2%; Pred. No. 7e-10;
tive 14; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.6%; Score 164.5; DB 2
41.2%; Pred. No. 2.1e-10;
tive 15; Mismatches 22
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A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                   apoptosis inhibitory protein - human
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Best Local Similarity 41.2
Matches 28; Conservative
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Best Local Similarity 41.2°
Matches 28; Conservative
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220 WFPKCEFL 227
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                                             N;Alternate names: NAIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:036CA5
C;Comment: This protein, a new member of the inhibitor of apoptosis protein family, play
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A;Note: sequence extracted from NCBI backbone (NCBIN:127014; NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV CiSpecies: Cydia pomonella granulosis virus CpGV CiSpecies: Cydia pomonella granulosis virus CpGV CiSpecies: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 CiAccession: A45679

Ricrok, N.B.; Clem, R.J.; Miller, L.K.
A; Virol. 67, 2186-2114, 1993

A; Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A; Reference number: A45679; MUID:93188168; PMID:8445726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
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                                                                                                                                                    kidney inhibitor of apoptosis protein - human ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("Spacession: JCT568 ("MulD: 21092523; PMID:11162435 ("Application family.") Apprecasion: JCT568 ("MulD: 21092523; PMID:11162435 ("Application family.") Apprecasion: JCT568 ("MulD: J092523; PMID:11162435 ("Application family.")
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llarity 47.8%; Pred. No. 2.1e-12;
Conservative 9; Mismatches 24; Indels
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Best Local Similarity 43.94
Matches 29; Conservative
                               329 WFPRCEFL 336
     99
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Best Local Similarity
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148 FPSCQFL 154
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A;Map position: 20q13.3
C;Keywords: apoptosis
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CYPGCKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-298 <LIN>
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A,Molecule type: DNA
A,Residues: 1-275 <CRO>
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RESULT 9

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C;Accession: T03183
R;Bahr, U.; Tidona, C.A.; Darai, G.
Vitus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693; PMID:9482589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus c.Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV c;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV c;Dacession: T10310 R;Antens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F. A,Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis A;Reference number: Z17011; MUD:97271300; PMID:9126251
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C; Species: Melanoplus sanguinipes entomopoxvirus
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C; Accession: T28409
B; A60080, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A; Reference number: Z20484; MUID:99102612; PMID:9847359
A; Accession: T28409
A; Accession: T28409
A; Accession: T28409
A; Accession: DAA
A; Molecule type: DAA
A; Residues: 1-150 cAFO>
A; Residues: 1-150 cAFO>
A; C; Genetics:
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A;Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94481.1; PID:g2738454
F;159-202/Domain: RING finger homology <RRN>
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                                                                                                  probable apoptosis inhibitor - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 15-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YEARIVTEGTWIYSV--NKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAK
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Best Local Similarity 36.4%; Pred. No. 6.4e-07;
Matches 24; Conservative 10; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.5%; Score 141; DB 2;
43.3%; Pred. No. 1.7e-08;
tive 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA.
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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Best Local Similarity
Matches 26; Conserv
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C;Species: Drosophila melanogaster
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accessor 505545
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C
EMBO J. 15, 2685-2694, 1996
A;Title: A conserved family of cellular genes related to the baculovirus iap gene and en A;Reference number: 869544; MUID:96256286; PMID:8654366
A;Accession: 869545
A;Status: preliminary; nucleic acid sequence not shown
A;Neeiques: preliminary; nucleic acid sequence not shown
A;Residues: 1-497 <br/>A;Occession: Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family Of Conserved Family 
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: $68452; $78528
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAF A;Title: Suppression: $68452
A;Accession: $68452
A;Accession: $68452
A;Accession: $60452
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A;Cross-references: UNIPROT:Q24307; EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g118
R;Baird, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, January 1996
A;Reference number: S78528
A;Accession: S78528
A;Accession: S78528
A;Accession: S78528
A;Accession: S78528
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
A;Cross-references: FlyBase:FBGn0015247
C;Function:
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A,Gene: ilp
C,Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F,446-490/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Description: apoptotic suppressor
C.Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C.Keywords: apoptosis; zinc finger
F;445-489/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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I Similarity 41.8%; Pred. No. 4.9e-09;
28; Conservative 12; Mismatches 25; Indels
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271 SPKCQFV 277
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Best Local S:
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A;Note: MSV248

Query Match 32.6%; Score 126; DB 2; Length 150; Best Local Similarity 33.3%; Pred. No. 6e-07; Matches 23; Conservative 14; Mismatches 26; Indels

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Search completed: October 22, 2004, 11:21:44 Job time: 25.1493 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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	earch time 84.7164 Seconds
OM protein - protein search, using sw model	October 22, 2004, 11:21:03 ; Search time 84.7164 Seconds
OM protein -	Run on:

Sequence: 1 VBARIVTFGTWIYSVNKEQL......KPSEDPWDQHAKCYPGCKYL 66
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 segs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/PCTT May PUB.pep:\*
3: /cgn2\_6/ptodata/2/pubpaa/NS06\_NEW\_PUB.pep:\*
4: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
5: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
6: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
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19: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description		Company 24 Appli	Semience 10 Appl	Segrence 10, Appl	Somione 10, Appl	Sequence 225, App	Sequence In, Appl	sequence 25, Appl	Sequence 25. Annl	Seminary of apprent	Iddy 'or company	seduence 4, Appil	Segmence 39. Anni	Comonos	edderice 4, Appri	sequence 4, Appli
COLUMNIES		qı	US-09-201-936-24	US-10-600-272-24	US-09-974-592-10	US-09-201-936-10	US-10-636-065-225	TIS-10-600-272-10				US-09-965-967-20		F-004 170 07 00	US-09-964-899-39	US-09-974-592-4	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	03-03-707-80-F
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14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60

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; SEQ ID NO 10
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-974-592-10
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Best Local Similarity
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US-10-636-065-225
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APPLICANT: Instrum, Peter
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Fang, Benjamin K
APPLICANT: Frang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DIEBASE
TITLE OF INVENTION: DIEBASE
TITLE OF INVENTION: DIEBASE
TITLE OF INVENTION: DIEBASE
TITLE OF INVENTION: DIEBASE
TITLE OF INVENTION: DIEBASE
FILE REFERENCE: 0789/1009004
CURRENT PILING DATE: 2001-10-09
FRIOR REPLICATION NUMBER: US 09/617,053
FRIOR APPLICATION NUMBER: US 08/800,929
FRIOR APPLICATION NUMBER: US 08/800,929
FRIOR APPLICATION NUMBER: US 08/800,929
FRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY 60
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     1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60
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                                                                                                                                                                                                                           US-10-600-2/2-24

Deblication No. US20040157232A1

Sequence 24, Application US/10600272

Publication No. US20040157232A1

GENERAL INFORMATION.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS

FILE REFERENCE: 07891/00306

CURRENT APPLICATION NUMBER: US/10/600,272

CURRENT APPLICATION NUMBER: US 09/011,356

PRIOR APPLICATION NUMBER: PCT/IB96/01022

PRIOR FILING DATE: 1998-02-04

PRIOR FILING DATE: 1995-08-05

PRIOR FILING DATE: 1995-08-05

PRIOR PRICATION NUMBER: US 08/576,956

PRIOR FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FEASTSEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 2: 45

LENGTH: 66
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Patent No. US20020120121A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                1 YBARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                                                             Gaps
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Length 496;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MacKenilk, Robert G.
APPLICANT: MacKenilk, Alexander E.
APPLICANT: MacKenilk, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT APLICATION NUMBER: 09/011,356
EARLIER APLICATION NUMBER: 09/10122
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1996-08-05
EARLIER FILING DATE: 1996-08-05
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/51,485
EARLIER APPLICATION NUMBER: 08/51,485
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Publication No. US20040127694A1
GENERAL INFORMATION:
APPLICANT: LaCasse, Eric
APPLICANT: Hacasse, Eric
APPLICANT: Holcik, Martin
APPLICANT: Holcik, Martin
APPLICANT: Aniq, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
     Query Match 100.0%; Score 386; DB 9; Best Local Similarity 100.0%; Pred. No. 7.9e-39; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 496
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; Sequence 10, Application US/09201936
; Publication No. US20020187946A1
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Matches

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Sequence 25, Application US/10600272 Publication No. US20040157232A1 GENERAL INFORMATION:
                 Publication No. US20020187946A1
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Best Local Similarity 95.5
Matches 63; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
IIILE OF INVENTION: MANMALIAN IAP GENE FAMILY, PRIMERS,
IIILE OF INVENTION: MANMALIAN IAP GENE FAMILY, PRIMERS,
IIILE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT APPLICATION NUMBER: US 09/101,356
PRIOR PILING DATE: 1096-02-04
PRIOR FILING DATE: 1996-02-04
PRIOR FILING DATE: 1996-08-05
PRIOR APPLICATION NUMBER: US 08/576,956
PRIOR FILING DATE: 1995-08-05
PRIOR PILING DATE: 1995-12-22
PRIOR PILING DATE: 1995-12-22
PRIOR PILING DATE: 1995-12-22
PRIOR PILING DATE: 1995-10-32
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PRIOR PILING DATE: 1995-10-32
PRIOR PILING DATE: 1995-10-32
PRIOR PILING DATE: 1995-08-04
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                 FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
FRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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US-10-636-065-225
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US-10-600-272-10
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Best Local Similarity
Matches 66; Conserv
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TITLE OF INVENTION:
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US-09-201-936-25
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GENERAL INVORMATION:
APPLICANT: Mockeniuk:
APPLICANT: Mackeniuk:
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APPLICANT: Mackeniuk:
APPLICANT: Mackeniuk:
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY,
TILE REPERENCE: 07891/003004
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SEQ ID NOS: 45
SEQ ID NOS: 45
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APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
ITILE OF INVENTION: MANALILAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: MANALILAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REPERENCE: 07891/003006
CURRENT APPLICATION NUMBER: US 09/011,356
PRIOR PILING DATE: 1996-02-04
PRIOR FILING DATE: 1996-02-04
PRIOR FILING DATE: 1996-02-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PARKEQ for Windows Version 4.0
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95.5%; Pred. No. 2.7e-37;
tive 1; Mismatches 2;
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95.5%; Pred. No. 2.7e-37;
tive 1; Mismatches 2
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Best Local Similarity 95.5
Matches 63; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-974-592-4
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US-09-964-899-39
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Best Local Similarity
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PGCKYL 66
                                        64 PGCKYL 69
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US-09-974-592-4
61
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                                                                                                                                                                                                                      Sequence 20. Application US/09965967

| Sequence 20. Application US/09965967
| Patent NO. US20020177557A1
| GENERAL INFORMATION:
| APPLICANT: Shi, Yigong
| TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
| TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
| TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
| TITLE OF INVENTION: 0011(01-1739-1)
| CURRENT FILING DATE: 2001-09-29
| PRIOR APPLICATION NUMBER: 60/236,574
| PRIOR APPLICATION NUMBER: 60/256,830
| PRIOR FILING DATE: 2000-12-20
| NUMBER OF SEQ ID NOS: 30
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: PatentIn version 3:1
| LENGTH: 107
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                               4 YEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWY
    YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
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94.8%; Score 366; DB 9; Length 107;
Best Local Similarity 95.5%; Pred. No. 4.5e-37;
Matches 63; Conservative 1; Mismatches 2; Indels
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; Sequence 4, Application US/10024433
; Publication No. US20020086409A1
; Publication No. US20020086409A1
; TITLE DE INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/10/024,433
; CURRENT FILING DATE: 1291-12-18
; PRIOR APPLICATION NUMBER: 09/239,867
; RICHARD APPLICATION NUMBER: 1999-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 236
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Best Local Similarity 95.5%; Pred. No. 1e-36;
Matches 63; Conservative 1; Mismatches
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US-10-024-433-4
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US-09-965-967-20
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                                                                       1 YEARIVIFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60
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Publication No. US20030224399A1
GENERAL INFORMATION:
FILLS OF INVENTION: Methods for Determining the Prognosis
TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
TITLE OF INVENTION: For Patients with a Prostate Neoplastic Condition
TITLE OF INVENTION: For Patients with a Prostate Neoplastic Condition
TITLE OF INVENTION: For Patients with a Prostate Neoplastic Condition
CURRENT PILLING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: US 60/356,956
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
                   0; Gaps
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95.5%; Pred. No. 2.3e-36;
Live 1; Mismatches 2; Indels
               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09201936
| Sequence 4, Application US/09201936
| Publication No. US2020187946A1
| SEMERAL INFORMATION:
| APPLICANT: Knochaluk, Robert G. |
| APPLICANT: MacKenzie, Alexander E. |
| APPLICANT: Baird, Stephen |
| APPLICANT: Liston, Peter G. |
| APPLICANT: Liston, Peter G. |
| TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, ITLE OF INVENTION: PROBES, AND DETECTION METHODS CURRENT FILING DATE: 1998-12-01
| CURRENT FILING DATE: 1998-12-04 |
| EARLIER FILING DATE: 1998-02-04 |
| EARLIER FILING DATE: 1996-08-05 |
| EARLIER FILING DATE: 1995-08-05 |
| EARLIER PELLING DATE: 1995-08-05 |
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   63; Conservative
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Best Local Similarity 95.57
Matches 63, Conservative
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ORGANISM: Homo sapiens
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Query Match

94.8%; Score 366; DB 14; Length 497;
Best Local Similarity 95.5%; Pred. No. 2.3e-36;
Matches 63; Conservative 1; Mismatches 2; Indels
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APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
ITILE OF INVENTION: Antisense IAP Nucleic Acids and Uses
ITILE OF INVENTION: Thereof
FILE REPERENCE: 07891/052005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT PILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR PILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSEQ for Windows Version 4.0
FRION 199
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94.8%; Score 366; DB 16;
Best Local Similarity 95.5%; Pred. No. 2.3e-36;
Matches 63; Conservative 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 219, Application US/10636065; Publication No. US20040127694A1; GENERAL INFORMATION: APPLICANT: Korneluk, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-636-065-219
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Sequence Sequence Sequence

JS-09-239-867-2

Sequence Sequence Sequence

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; Search time 28.0746 Seconds (without alignments) 155.905 Million cell updates/sec
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1 YEARIVTFGTWIYSVNKEQL......KPSEDPWDQHAKCYPGCKYL
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                 OM protein - protein search, using sw model
                                                                                                        October 22, 2004, 11:08:12
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                  Copyright
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Perfect score:
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seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Issued Patents AA:\*
1: /cgn2\_6/ptodata/1/iaa/sA\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/sB\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/sA\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/sB\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/pcTUS\_COMB.pep:\* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Sequence 10, Sequence 10, Sequence 10, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence US-08-511-485-24 US-09-201-936-24 US-09-201-935-24 US-08-511-485-10 US-08-511-485-10 US-08-511-485-10 US-09-201-936-10 US-09-617-053A-10 US-09-617-053A-10 US-09-201-936-10 US-09-201-936-10 US-09-201-936-10 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 US-09-201-936-25 DB Query Match Length 100.0 100.0 100.0 100.0 100.0 100.0 100.0 94.8 94.8 Result М М 

· 0 Appl Appl Appl Appl Appl Appl Gaps 26, 58, Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence ., 0 Length 66; 100.0%; Score 386; DB 2; Length 6 100.0%; Pred. No. 3.8e-43; Live 0; Mismatches 0; Indels APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Markenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CORRESPONDENCE. ADDRESS: CITY: bo.
STATE: MA
COUNTRY: UGA
COMPUTER READABLE FORM:
MEDLIUM TYPE: FORDAY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
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REFERENCE/DOC US-08-657-759-19 US-08-975-080-29 US-08-975-080-29 US-08-975-080-32 US-08-511-485-26 US-09-201-936-26 US-09-201-936-26 US-09-201-936-26 US-09-201-936-26 US-09-201-936-26 US-09-212-971-6 US-09-212-971-6 US-08-569-749-4 US-09-617-053A-6 ALIGNMENTS ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street Sequence 24, Application US/08511485 Patent No. 5919912 GENERAL INFORMATION: Ouery Match 100.0 Best Local Similarity 100.0 Matches 66; Conservative MOLECULE TYPE: protein TOPOLOGY: both STRANDEDNESS: US-08-511-485-24 US-08-511-485-24 RESULT 1

09 1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY

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Sequence 4, 1 Sequence 4, 1 Sequence 219, Sequence 4, 1

US-09-672-717-219

US-09-201-932-4

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence

US-09-212-971-4 US-08-800-929A-4

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TYPE: PRT
CORGANISM: Mus musculus
US-09-201-932-24
                   TYPE: PRT
; ORGANISM: Mus musculus
US-09-011-356-24
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US-09-201-932-24
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1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60
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100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels
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US-Gquence 24, Application US/09011356A

Patent No. 6656704

GENERAL INPORMATION:

APPLICANT: Morematic, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Pates, AND DETECTION METHODS

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE REFERENCE: 07691/003002

CURRENT APPLICATION NUMBER: US/09/011,356A

CURRENT APPLICATION NUMBER: US/09/01022

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER FILING DATE: 1995-08-05

EARLIER FILING DATE: 1995-12-22

EARLIER FILING DATE: 1995-12-22

EARLIER FILING DATE: 1995-08-04

MUMBER OF SEQ ID NOS: 45

SOFTWARRE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                  US-09-201-936-20

US-09-201-936-20

US-09-201-936-20

Sequence 24, Application US/09201936

Patent No. 6541457

GENERAL INPORMATION:

APPLICANT: MacKenzie, Alexander E.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: Liston, Peter

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMER

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMER

TITLE OF INVENTION: MAMMER: US/09/201,936

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/011,356

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1995-08-05

EARLIER FILING DATE: 1995-08-05

EARLIER FILING DATE: 1995-08-05

EARLIER FILING DATE: 1995-08-05

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45-

SEQ ID NO 24

LENGTH: 66

LENGTH: 66
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US-09-011-356-24
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                                                                                                                       1 YEARIVIFGIWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLIDWKPSEDPWDQHAKCY
                                                              Gaps
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Query Match
100.0%; Score 386; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.8e-43;
Matches 66; Conservative 0; Mismatches 0; Indels
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APPLICANT: Korneluk, Robert G.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: MacKenzie, Alexander E.

APPLICANT: MacKenzie, Alexander E.

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, TITLE OF INVENTION: PROBES, AND DETECTION METHODS NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORMATION,
GENERAL INCORMATION,
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT APPLICATION NUMBER: 08/09/201,932A
CURRENT FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER PILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE PREACTER PROBESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 386; DB 4;
100.0%; Pred. No. 3.8e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 24, Application US/09201932A; Patent No. 6689562; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/08511485; Patent No. 5919912
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Best Local Similarity 100.0
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Query Match
Best Local Similarity 100.0
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                 324 PGCKYL 329
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              ; ORGANISM: MUB
US-09-212-971-10
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APPLICANT Korneluk, Robert G
APPLICANT MACKEALLE, Alexander E
APPLICANT MACKEALLE, Alexander E
APPLICANT MACKEALLE, Alexander E
APPLICANT Histon, Peter
APPLICANT Histon, Peter
APPLICANT Fasng, Benjamin K
APPLICANT Fasng, Benjamin K
APPLICANT Franc, Christine
ITITLE OF INVENTION: DISEASE
ITITLE OF INVENTION: DISEASE
ITITLE OF INVENTION: DISEASE
ITITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
ITITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
ITITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATION
ITITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: 09/017,354
EARLIER APPLICATION NUMBER: 09/017,354
EARLIER PILING DATE: 1996-04-26
EARLIER PILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 YEARIVIFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDFWDQHAKCY 323
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                                                                                            COMPUTED: USAN
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-006/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
FILING DATE: 04-AUG-1995
ATCORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
PREFRENCE/DOCKET NUMBER: ...
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09212971B Patent No. 6107041
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0754
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 minn acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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Best Local Similarity 100.0
Matches 66; Conservative
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; MOLECULE TYPE: protein
US-08-511-485-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: not
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         STREET: STREET
                                                                                          COUNTRY:
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APPLICANT: MacKenzie, Alexander G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Baird, Stephen
APPLICANT: Tang, Beird
APPLICANT: Tang, Berjamin K
APPLICANT: Tang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TORRESPONDENCE ADDRESS:
ADDRESSE: Clark & Elbing LLP
STEET: 176 Federal Street
                                                          0
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                                                                                                                                  1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY
                                                          Gaps
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     Length 496;
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100.0%; Score 386; DB 3;
100.0%; Pred. No. 4.4e-42;
ive 0; Mismatches 0;
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100.0%; Score 386; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.4e-42;
Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07891/009001
                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08800929A
Patent No. 6133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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FILE REFERENCE: 07891/02500
; SEQ ID NO 10; LENGTH: 496; TYPE: PRT (CREALISM: MUS musculus US-09-201-936-10
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APPLICANT: Korneluk, Robert G
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Rephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Brang, Benjamin K
APPLICANT: Pract, Christine
ITILE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
ITILE OF INVENTION: DISEASE
ITILE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-13
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                                          264 YEARIVTFGTWITSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 323
       1 YEARIVTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWDQHAKCY 60
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Best Local Similarity 100.0%; Pred. No. 4.4e-42;
Matches 66; Conservative 0; Mismatches 0; Indels
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APPLICANT: MorChaluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: BacKenzie, Alexander E.
APPLICANT: BacKenzie, Alexander E.
APPLICANT: BacKenzie, Alexander E.
APPLICANT: Backenzie, Alexander E.
APPLICANT: Liston, Peter
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE REPRENCE: 07891/003003
TITLE REPRENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
GERLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: POT/1896/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER APPLICATION NUMBER: 1995-09-04
NUMBER: OF SEQ ID NOS: 45
NUMBER: PastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09617053A Patent No. 6300492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-617-053A-10
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US-09-201-936-10
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  Length 496;
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US-09-011-356-10

US-09-011-356-10

Sequence 10, 6655704

Parent No. 6655704

GENERAL INCORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Liston, Peter
TITLE OF INVENTION: MarmallaN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MarmallaN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MARMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MARMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MARMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION WINDER: US/09/011,356A

CURRENT APPLICATION NUMBER: PS/11996/01022

BARLIER FILING DATE: 1996-09-14

EARLIER FILING DATE: 1996-08-05

BARLIER FILING DATE: 1996-08-05

BARLIER FILING DATE: 1995-12-22

BARLIER FILING DATE: 1995-12-22

BARLIER FILING DATE: 1995-12-22

SARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

SEQ ID NO 10
                                                          Indels
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APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
IIILE OF INVENTION: Thereof
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Best Local Similarity 100.0%; Pred. No. 4.4e-42;
Matches 66; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 386; DB 4; Best Local Similarity 100.0%; Pred. No. 4.4e-42; Matches 66; Conservative 0; Mismatches 0;
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US-09-672-717-225
Sequence 225, Application US/09672717
; Patent No. 6673917
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APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Bric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
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RESULT 14
US-09-201-936-25
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Sequence 10, Application US/09201932A

GENERAL INFORMATION:
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Latton, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMER: US/09/201,932A
CURRENT APPLICATION NUMBER: US/09/201,932A
CURRENT FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: OF/1B96/01022
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                    100.0%; Score 386; DB 4;
100.0%; Pred. No. 4.4e-42;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SEQ TYARRE: PastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 496
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Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 66; Conservative 0
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US-09-201-932-10
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Best Local Similarity
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US-09-201-932-10
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APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SECURICES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09201936;
Patent No. 6541457;
GENERAL INFORMATION:
APPLICANT: MacKenzie, Alexander E.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baixd, Stephen
APPLICANT: Baixd, Stephen
APPLICANT: Inston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REPERENCE: 07891/003003
CURRENT FILMS DATE: 1998-12-01
FARLIER APPLICATION NUMBER: 09/011,356
EARLIER PILING DATE: 1998-02-04
EARLIER PILING DATE: 1998-02-06-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
NUMBER OF SEQ ID NOS: 45
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Best Local Similarity
Matches 63; Conserva
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94.8%; Score 366; DB 4; Length 66;
Best Local Similarity 95.5%; Pred. No. 1.6e-40;
Matches 63; Conservative 1; Mismatches 2; Indels
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US-09-011-356-25

Sequence 25, Application US/09011356A

Patent No. 6656704

GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN ISPECTION METHODS
FILE REFERENCE: 07891/003002

CURRENT APPLICATION NUMBER: US/09/011,356A

CURRENT FILING DATE: 1998-09-14

EARLIER FILING DATE: 1998-08-15

EARLIER FILING DATE: 1995-12-22

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 25

LENGTH: 66

LENGTH: 66

LENGTH: 66

LENGTH: 66
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; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 25; LENGTH: 66
                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-201-936-25
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October 22, 2004, 10:44:01; Search time 116.716 Seconds (without alignments) 208.999 Million cell updates/sec Run on:

US-09-654-743-27 402 Title: Perfect score:

1 HAARMRIFMYWPSSVPVQPE.....ESGDDFWVEHAKWFPRCEFL Scoring table: Sequence:

68

2002273 seqs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB R

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Score	402	402	402	393	393	393	393	393	393	393	393	393	393	393	393	393	393	366	366	366	360	360	340	340	0.70	
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AAW19582 AAW19747 AAW13546 AAW5295 AAY52703 AAX33997 ABG65664 ABU07431	ADB80948 AAE39811 ADG87135 ADH74643	AAU97837 ADL93367 ADO26542 AAB50694	AAW69298 ABP72155 ABG65667
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## ALIGNMENTS

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(AAMY9581-86) are a new class of mammalian proceins that are inhibitors of apoptosis (IAP) and which are characterised by the presence of a ring zinc finger domain (see also AAM19581) and at least one BIR (baculovirus IIAP repeat) domain (see also AAM19588). The HIAP amino acid sequences were deduced from cDNA clones (AAT7083) and AAT70838) from a human liver library. TAP polypeptides can be expressed in host cells (in vitro or in vivo) and used in methods for treating diseases and disorders involving apoptosis, esp. in a human diagnosed as HIV-positive or as having AIDS, a neurodegenerative disease, a myelodysplastic syndrome or an ischaemic injury, seleted from myocardai infarction, stroke, reperfusion injury, or a toxin-induced liver disease.
HIAP-1 and HIAP-2 and murine M-XIAP, M-HIAP-1 and M-HIAP-2
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 618 AA;
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269 HAARMRTEMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 328 1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK Length 618; Indels 100.0%; Score 402; DB 2; 100.0%; Pred. No. 9.2e-39; ive 0; Mismatches 0; Best Local Similarity 100. Matches 68; Conservative 329 WFPRCEFL 336 61 WFPRCEFL 68 Query Match à ð 셤 셤

RESULT 3

0

Gaps

0;

AAW69296 standard; protein; 618 13-NOV-1998 AAW69296; RESULT 2 AAW69296

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Human HIAP-2 protein. 

Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; HIAP-2 protein.

Homo sapiens

WO9835693-A2 20-AUG-1998 98WO-IB000781. 13-FEB-1998;

13-FEB-1997;

97US-00800929.

(UYOT-) UNIV OTTAWA

Pratt Baird S, Tsang B, Liston P, Mackenzie AE, WPI; 1998-467164/40. Korneluk R,

N-PSDB; AAV55040.

Inducing or NAIP po

Disclosure; Fig 3; 147pp; English.

Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving p53 mutations.

This sequence is the human HIAP-2 protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharnyx, thyrold, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity

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or NAIP
                                                                        antisense
to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIF genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors
                                                                                                                                                                                                                         1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
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100.0%; Pred. No. 9.2e-39;
iive 0; Mismatches 0;
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cancer; ovarian cancer; adenocarcinoma; lymphoma; IAD; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; cytostatic; Human inhibitor of apoptosis, HIAP2 ABG65665 standard; protein; 618 AA. proliferative disease. 26-AUG-2002 ABG65665; ABG65665

28-SEP-2000; 2000US-00672717. 27-SEP-2001; 2001WO-CA001379 (UYOT-) UNIV OTTAWA WO200226968-A2. Homo sapiens 04-APR-2002 

ŝ Young Holcik M, Baird S, ŭ Lacasse WPI; 2002-479562/51. N-PSDB; ABK93871 Korneluk RG,

AEGERA THERAPEUTICS INC.

(AEGE-)

enhancing

Novel antisense inhibitor of apoptosis nucleic acid useful for en apoptosis in a cell, for treating cancer and other proliferative

Disclosure; Fig 3; 135pp; English. diseases.

οŧ The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptosic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer.

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               sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autonommune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP
                                                                                                                                                                                                                                                                                                          269 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 328
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100.0%; Pred. No. 9.2e-39;
ive 0; Mismatches 0;
   IAP antisense molecule is useful to treat,
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Best Local Similarity
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baculovirus inhibitor of apoptosis repeat domain, BIR domain, apoptosis pathway; embryonic development; viral pathogenesis; cancer; autoimmune disorder; neurodegenerative disease; apoptotic response; systemic lupus erythematosis; multiple sclerosis; viral infection; herpes virus; poxvirus; adenovirus; inhibitor of apoptosis; IAP; HIAP1; cIAP2; HIAP2; cIAP1; RING zinc finger; caspase-3; caspase-7; caspase-9; cytostatic; neoplasm; leukaemia; colon carcinoma; cervical cancer; uterine cancer; testicular cancer; small cell lung carcinoma; uterine cancer; renal cell carcinoma; Wilm's tumour; human; BIR 3 domain. Human inhibitor of apoptosis (IAP) protein HIAP2 BIR3 domain.

04-DEC-2003 (first entry)

Homo sapiens,

WO2003040172-A2

15-MAY-2003

12-NOV-2002; 2002WO-CA001738.

2001US-0332300P. 09-NOV-2001; 08-APR-2002; (AEGE-) AEGERA THERAPEUTICS INC.

Korneluk RG,

Boudreault A,

Liston

La Casse E,

WPI; 2003-513532/48.

Polypeptide capable of forming a complex with a polypeptide comprising a baculovirus inhibitor of apoptosis repeat domain useful for treating cancer and other neoplasms

Disclosure, Fig 1A; 53pp; English.

This invention relates to a substantially pure polypeptide having a length of less than 100 amino acids and capable of forming a complex with a polypeptide that includes a baculovirus inhibitor of apoptosis repeat (BIR) domain. The apoptosis pathway is known to play a critical role in embryonic development, viral pathogenesis, cancer, autoimmune disorders 

Human inhibitor of apoptosis 1 (hIAP-1) (AAW04583) is a protein useful for treating degenerative diseases, rheumatoid arthritis, septic shock,

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been implicated in the development of cancer, autoimmune disorders (for example systemic lupus erythematosis and multiple sclerosis) and viral confections (including herpes virus, poxvirus and adenovirus. The inflictions of apoptosis (IAPS) are a family of proteins possessing one or ciractions including herpes virus, poxvirus and adenovirus. The inhibitors of apoptosis (IAPS) are a family of proteins possessing one or ciracian and HIAP2 (IAP1) all posses three BIR domains and carboxy terminal RING zinc fingers. The IAPS bind and inhibit caspases -3, -7 and -9 which are proteases involved in the initiation of apoptosis. Compounds which inhibit the activity of IAPS may therefore have cytostatic activity through the enhancement of apoptosis. The polypeptides of the invention are candidate peptide ligands for binding to the BIR domain of IAPs. They may be useful for the treatment of cancer and other neoplasms, such as leukamans, colon carcinoma, cervical cancer, uterine cancer, testicular cancer, small cell lung carcinoma, uterine cancer, testicular and wilm's tumour, and for enhancing apoptosis. The present sequence is that of the human inhibitor of apoptosis (IAP) protein HIAP2 BIR3 domain concerded and wilm's tumour, and for enhancing apoptosis.
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   The failure of the apoptotic response has
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    useful for

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treating degenerative diseases, as antiviral defence mechanism and
preventing cell death during trauma and strokes.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 68;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 393; DB 7;
Pred. No. 8.9e-39;
0; Mismatches 1;
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 neurodegenerative diseases.
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les 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                 Sequence 68 AA;
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7.7e-38;

98.5%;

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                                                                                                                                                                                                                                                   89 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 148
                                                                                                                                                                                                                                 60
as an antiviral defence mechanism, and for preventing cell death during strokes or trauma. Its amino acid sequence was deduced from a CDNA clone (AAT43709) that can be obtd. from human Jurkat cell lines or human osteoclastoma stromal cell lines. Recombinant hIAP-1 can be produced in prokaryotic or eukaryotic host cells, or expressed in vivo. It can also be used to screen for modulators of hIAP-1 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitor of apoptosis; CIAP1; apoptosis; cancer; leukaemia; lymphoma; neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
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                                                                                                                                                            Score 393; DB 2; Length 43
Pred. No. 7.3e-38;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              ABP72158 standard; protein; 459 AA
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1 Similarity 98.5%;
67; Conservative
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Matches 67;
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97.8%; Score 393; DB 6; Length 459;

Sequence 459 AA;

Query Match

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Mammalian IAP homologue B (MIHB) (AAW19746) is a human homologue of baculovirus inhibitor of apoptosis protein (IAP). Its amino acid sequence was deduced from a cDNA clone (see also AAT72711) isolated from a human foetal liver cDNA library using primers based on human EST sequences that resembled the BIR repeats of Crygia pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also AAW19745 and AAW19747-25) and their derivatives and chemical analogues can be used in methods for modulating apoptosis in animal cells, specifically for treatment, by inhibition, of degenerative and infectious disease or, by promotion, of cancer and autoimmune disease
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                                                    269 HAARMKTFMYWPSSVFVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
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                                   1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
                                                                                                                                                                                                                                                                                            Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHB; degenerative disease; infectious disease; autoimmune disease; cancer;
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated protein homologues of viral inhibitors of apoptosis - used modulate apoptosis for treatment of degenerative, infectious or
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            Indels
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Pred. No. 1.1e-37;
Pred. No. 7.7e); Mismatches
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/label= RING finger
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/label= BIR
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/label= BIR
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/label= BIR
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Best Local Similarity 98.5
Matches 67; Conservative
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Best Local Similarity
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Human cellular inhibitor of apoptosis-1 sequence.

26-NOV-1999

AAY33998;

Cellular Inhibitor of

AAY33998 standard; protein; 618 AA.

AAY33998

329 WFPRCEFL 336

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us-09-654-743-27.rag

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                                                The human cellular inhibitor of apoptosis proteins (c-IAPI/2 - AAT61590/T61591) comprise a series of defined structural domain repeats and/or a RING finger domain, in particular, at least two of a first domain repeat (AAM1354) or ascond domain repeat (AAM1354) or AAM13550, and a third domain repeat (AAM13551 or AAM13552) and/or a RING finger domain (AAM13553 or AAW13554), or a consensus sequences derived from these human genes. The nucleic acid is used for recombinant prodn. The human cellular inhibitor of apoptosis protein which modulates apoptosis regulation. The nucleic acids are useful in therapies where increased cell-specific apoptosis at desired, e.g. in restinosis, increased.
                             1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding cellular inhibitor of apoptosis proteins - useful for apoptosis regulation in cells to reduce or increase apoptosis and for pharmacological screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease states, myocardial infarction, glomerular nephritis, transplant rejection and infectious diseases, e.g. HIV. They can also be used in conditions requiring a reduction in apoptosis
         Gaps
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                                                                                                                                                                                                                                                                                                                           IAP; inhibitor; apoptosis; RING finger domain; restinosis; myocardial infarction; nephritis; HIV.
      1; Indels
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 18-20; 35pp; English.
                                                                                                                                                                                                 AAW13545 standard; protein; 618 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00512946.
95US-00569749.
                                                                                                                                                                                                                                                                (first entry)
 67; Conservative
                                                                                                                       329 WFPRCEFL 336
                                                                                          WFPRCEFL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TULA-) TULARIK INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-154209/14.
N-PSDB; AAT61590.
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 618 AA;
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                22-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-1995;
08-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      WO9706182-A1
                                                                                                                                                                                                                                                                                               Human c-IAP1
                                                                                            61
                                                                                                                                                                                                                                AAW13545;
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Matches
                                                                                                                                                                   RESULT 8
                                                                                                                                                                                   AAW13545
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The invention provides antisense compounds of 8-30 nucleotides that inhibit the expression of human Cellular Inhibitor of Apoptosis-1 (c-IAP-1). The antisense compounds may be used for diagnostics, therapeutics (for modulating the expression of c-IAP-1), prophylaxis (e.g. to prevent or delay infection, inflammation, or tumor formation), as research and in kits. The present sequence members of a biological pathway) of apoptosis-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 HAARMRITEMYWPSSVEVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVEHAK 60
                                                                             Apoptosis-1; antisense; diagnostic; therapeutic; infection; inflammation; tumor formation.
                                                                                                                                                                                                                                                                                                                                    Antisense compounds complementary to Cellular Inhibitor of Apoptosis-1 useful for e.g. diagnostics, therapeutics, and as research reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.8%; Score 393; DB 2; Length 61
98.5%; Pred. No. 1.1e-37;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human inhibitor of apoptosis protein XIAP.
                                                                                                                                                                                                                                                                        멼.
                                                                                                                                                                                                                                                                                                                                                                        Example 13; Col 41-46; 32pp; English.
                                                                                                                                                                                                                                                                        Ackermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP72160 standard; protein; 618 AA.
                                                                                                                                                                                            98US-00205204.
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                                                                                                                                                                                                                                                                      Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 98.5
67; Conservative
                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                         c-IAP-1; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 WFPRCEFL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
                                                                                                                                                                                                                                                                                              WPI; 1999-561047/47.
                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ22143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 618 AA;
                                                                                                                  Homo sapiens,
                                                                                                                                                                                            03-DEC-1998;
                                                                                                                                                                                                                   03-DEC-1998;
                                                                                                                                                                                                                                                                    Bennett CF,
                                                                                                                                                                  28-SEP-1999,
                                                                                                                                                                                                                                                                                                                                   Antisense
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Best Local 3
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61 WFPRCEFL 68

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1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK

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                                                                                                                                                                                                                                                                                                                                                                                                                                        appoposis protein XIAP. The invention provides a nucleic acid, such as an appoposis protein XIAP. The invention provides a nucleic acid, such as an antisense oligonucleotide, which specifically hybridises to a nucleic acid encoding an inhibitor of apportein, especially MIAPP, MIAP2, and encoding an inhibitor of apportein, especially MIAPP, Clay, CIAP1, CIAP2 and XIAP. A claimed method for inducing a cell's death comprises contacting the cell with the nucleic acid under conditions permitting the nucleic acid to enter the cell, especially the use of a vector, liposome, or a mechanical or electrical means. The method is used to treat acute lymphocytic leukaemia, acute myelogenous leukaemia, lung cancer, breast cancer, ovarian cancer, prostate cancer, lymphoma, Hodgkin's disease, malignant melanoma, neuroblastoma, renal calcinoma and squamous cell carcinoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 HAARMETFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RING-SH 3, Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60; Hsp70; Hsp90, STAM1; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsg101; cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomyopathy.
                neuroblastoma; carcinoma; melanoma; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
Inhibitor of apoptosis; XIAP; human; apoptosis; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of human inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 393; DB 6; Length 61
Pred. No. 1.1e-37;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RING-SH complex related protein, SEQ ID No 23.
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 18A; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 618 AA.
                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.8%;
                                                                                                                                                                                         03-JUL-2001; 2001US-00898158.
                                                                                                                                                         03-JUL-2002; 2002WO-US021002.
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                                                                                                                                                                                                                                                             Shelanski ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhabdovirus; filovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFPRCEFL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFPRCEFL 68
                                                                                                                                                                                                                                                                                             2003-210351/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003033646-A2.
                                                                                                                                                                                                                                                                                                             N-PSDB; ABZ58105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 618 AA;
                                                                                         WO2003004606-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003
                                                       Homo sapiens.
                                                                                                                       16-JAN-2003
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                     lymphoma;
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24-APR-2003

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The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PI3K, actin, myosin, Hsp60, Hsp90, STRM12, STRM2A, STRMM2B, WIS-UIM, a GTPASE, an EZ enzyme, tsg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for identifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhabdoviruses, or filoviruses. This sequence is a protein comprising the RING-SH complex of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 HAARNKIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAP1; inflammatory response; rheumatoid arthritis; LTbetaR; lymphotoxin-beta receptor; modulator; cancer; immunological disease; apoptosis; cytostatic; immunosuppressive; antirheumatic; antiarthritic; antiinflammatory; dermatological; nephrotropic; antithyroid; thyromimetic; muscular Gen; neuroprotective; antianaemic; haemostatic;
                                                                                                                                                                                                         New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVEHAK
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                                                                                                                             Moskowitz H, Reiss Y, Alroy I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR84600 standard; protein; 618 AA.
                                                                                                                                                                                                                                                                                                 Example 2; Fig 23; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2003; 2003WO-US003923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2002; 2002US-0355183P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.8%;
Best Local Similarity 98.5%;
Matches 67; Conservative
            31-JUL-2002; 2002WO-US024589.
                                            31-JUL-2001; 2001US-0308958P.
09-NOV-2001; 2001US-0345846P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vasotropic; antidiabetic.
                                                                                               (PROT-) PROTECLOGICS INC.
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                                                                                                                                                               WPI; 2003-393509/37.
N-PSDB; ADB80990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 618 AA;
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                                                                                                                                                                                                                                                                   or filoviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAP1 protein.
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                                                                                                                                Greener T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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(AMHP ) WYETH.

Qiu Y, Nickbarg EB, Wooters JL,

WPI; 2003-748125/70.

New purified lymphotoxin-beta receptor protein complex, useful for identifying modulators of lymphotoxin-beta receptor activity or expression for treating or preventing cancer or an autoimmune disorder, vasculitis or diabetes.

Disclosure; Page 7; Opp; English.

The present invention relates to a purified complex comprising a lymphotoxin beta receptor (ITbetaR) polypeptide and Smac polypeptide. The Numbhotoxin beta receptor (ITbetaR) complex is useful for identifying modulators of ITbetaR activity or expression for treating or preventing cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's disease, Hashimoto's thyroditis, pemphigus vulgaris, myasthenia gravis, purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's syndrome, ankylosing spondylitis, vasculitis, or type I diabetes mellitus. The present sequence is an IAPI protein, which forms part of the complex of the invention

Sequence 618 AA;

1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK Gaps .; 0 97.8%; Score 393; DB 7; Length 618; 98.5%; Pred. No. 1.1e-37; live 0; Mismatches 1; Indels Conservative 329 WFPRCEFL 336 68 Local Similarity 61 WFPRCEFL 67; Query Match Matches g ò 셤

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ADD25639 standard; protein; 618 AA. ADD25639; RESULT 13 ADD25639 

(first entry)

15-JAN-2004

Binding domain-immunoglobulin fusion protein-associated protein #97.

CH2 constant region; CH3 constant region; IgG; ..., antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease. Binding domain, immunoglobulin, fusion protein, cytostatic, antiarthritic, immunosuppressive, antidiabetic, antithyroid, neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1;

Unidentified

US2003118592-A1

25-JUL-2002; 2002US-00207655.

17-JAN-2001; 2001US-0367358P. 17-JAN-2002; 2002US-00053530. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P.

(GENE-) GENECRAFT INC

Thompson PA; Hayden-Ledbetter MS,

WPI; 2003-801317/75

New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

Disclosure; SEQ ID NO 200; 157pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comparising a binding domain polypeptide that is fused to an immunoglobulin heavy chain comparison polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the full a constant region polypeptide. The hinge region polypeptide comprises: a wild-type human iggl immunoglobulin hinge region polypeptide derived from (a) having 30 more cysteine residue; where the mutated human iggl immunoglobulin hinge region polypeptide derived from (a) having 30 more cysteine residues; where the first cysteine is not mutated; when it mannoglobulin hinge region polypeptide comprises; a wild-type human iggl immunoglobulin hinge region polypeptide comprises; where the mutated human iggl immunoglobulin hinge region polypeptide contains or cysteine residue; where the first cysteine is not mutated; when it is a mannoglobulin hinge region polypeptide contains or cysteine residue; and a mutated human iggl immunoglobulin hinge region polypeptide contains or cysteine residues. The hinding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The hinding domain-immunoglobulin hinge region polypeptide contains or pysteine residues. The hinding domain-immunoglobulin hinge region polypeptide contains or cysteine residues. The hinding domain-immunoglobulin hinge region polypeptide contains or suppersed to elimunoglobulin fusion protein, a recombinant expression changes and included are an isolated polymucleotide complication or a promoter, construct, producing the binding domain-immunoglobulin fusion protein, a recombinant expression or pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a recombinant condition or a g-cell composition comprising the binding domain-immunoglobulin fusion protein or pharmaceutical composition comprising the binding domain-immunogl

Sequence 618 AA; 

. Length 618; 1; Indels 97.8%; Score 393; DB 7; 98.5%; Pred. No. 1.1e-37; 0; Mismatches 67; Conservative Query Match Best Local Similarity Matches

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1 HAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK

임 δ RESULT 14

ADG10748 standard; protein; 618 AA. ADG10748 SAXB

ADG10748;

(first entry)

12-AUG-2004

ADP65159;

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STATE-activating proteins and encoded genes, applicable in diagnosis of and developing drugs to treat allergic diseases, inflammations, autoimmune diseases, diabetes, hyperlipidemia, infections e.g. HIV, and
                                                       allergic disease, inflammation, autoimmune disease, diabetes, hyperlipidaemia; cancer; infection; HIV infection; human immunodeficiency; cancer; Thi hyperfunction; antiallergic; antiinflammatory; antidiabetic; antilipaemic; antiinfective; anti-HIV; cytostatic.; gene therapy; antisense therapy; ribozyme therapy.
                                            STAT6-activating protein; drug screening; activator; inhibitor;
                                                                                                                                                                                                                                                                                                      Honda G, Matsuda A, Muramatsu S, Ishizawa K;
                      Human STAT6-activating protein, SEQ ID NO:338.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1, SEQ ID NO 338; 2080pp; Japanese.
                                                                                                                                                                                                                               25-MAY-2001; 2001JP-00157043.
30-AUG-2001; 2001JP-00260681.
                                                                                                                                                                                                                                            30-AUG-2001; 2001JP-00260681.
10-OCT-2001; 2001JP-00313175.
                                                                                                                                                                                                                                                                                (ASAH ) ASAHI KASEI KOGYO KK.
                                                                                                                                                                                                      22-MAY-2002; 2002WO-JP004949
(first entry)
                                                                                                                                                                                                                                                                                                                               WPI; 2003-140442/13.
N-PSDB; ADG10747.
                                                                                                                                                           WO200296943-A1
                                                                                                                                   Homo sapiens.
 26-FEB-2004
                                                                                                                                                                                  05-DEC-2002.
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The invention relates to 242 human STAT6-activating proteins and cDNAs encoding them (ADG10411-ADG10894) and to sequences with 95% or more homology to the STAT6-activating proteins and their encoding nucleic acids. The invention also relates to recombinant vectors and host cells comprising a STAT6-activating protein-encoding nucleic acid; the recombinant production of a STAT6-activating protein; an antibody specific for a STAT6-activating protein; antisense oligonucleotides and ribozymes targeted to nucleic acids encoding a STAT6-activating protein; antisense oligonucleotides and ribozymes targeted to nucleic acids encoding a STAT6-activating enchods of screening for activators or inhibitors of STAT6-activating nucleic acids encoding them, and modulators of their activity or expression are useful in the diagnosis and treatment of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidaemia, cancer, infections (e.g., HIV) cancer and disorders associated with Thi hyperfunction. The present sequence is related to the invention. proteins; drug compositions comprising a modulator of STAT6-activating protein activity or expression; and methods of treating patients by administration of the drug compositions. The STAT6-activating proteins,

Sequence 618 AA;

Query Match

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0
                                                                                            269 HAARMETFWYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
                                                                        1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
                                         Gaps
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0
97.8%; Score 393; DB 7; Length 61
98.5%; Pred. No. 1.18-37;
iive 0; Mismatches 1; Indels
                     Local Similarity 98.5
nes 67; Conservative
                         Best Loc
Matches
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Length 618;

WFPRCEFL 336 329 RESULT 15 q

WFPRCEFL 68

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ADP65159 standard; protein; 618 AA. ADP65159

Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and autoimmune disease; arthritide; gene expression analysis; rheumatic; antiarthritis; collagen-induced; immunosuppressive; antiarheumatic; antiarthritic; osteopathic; antigout; antinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyadja; osteoarthritis; gout; juvenile rheumatoid arthritis; Human baculoviral IAP repeat-containing protein 2, cIAP1, hiap-2. (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. 31-OCT-2001; 2001US-0336220P 31-OCT-2002; 2002WO-US035433 Thorton SL; WPI; 2003-712740/67. GENBANK; NP 001157. WO2003072827-A1. immune; human Homo sapiens. 04-SEP-2003 Hirsch R, 

patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that that results in a gene expression signature of the mRNA, and using that that results in a gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of further comprises: a treatment of rheumatoid arthritis; identification of cher than a mouse; diagnosis of rheumatoid arthritis; in a mammal other than a mouse; diagnosis of rheumatoid arthritis; in a mammal of array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of a utoimmune disease or rheumatoid arthritis; streening the efficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis, and reducing the symptoms associated with collagentinduced arthritis, and reducing the symptoms associated with collagentinduced arthritis, and reducing the symptoms associated with collagentinduced arthritis, and reducing the symptoms associated with collagentinduced arthritis, and reducing the symptoms are useful for methods and compositions of the present invention are useful for catigoria, antidosing and treating autoimmune disease caused by an infectious agent. This sequence represents a rhematoid arthritis, lupus, ankylosing spondylitis, fibrositis, or immune diseases caused by an infectious agent. This sequence represents a mour he specification. It has been supplied in an electronic format from The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a Disclosure; Page; 56pp; English.

Sequence 618 AA;

.; 0 Length 618; ch 97.8%; Score 393; DB 7; Length 61. I Similarity 98.5%; Pred. No. 1.1e-37; 67; Conservative 0; Mismatches 1; Indels Query Match Best Local S Matches

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9 1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 

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269 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328

61 WFPRCEFL 68 |||||||| 329 WFPRCEFL 336

95 Ag

Search completed: October 22, 2004, 11:16:33 Job time: 117.716 secs

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Best Local Similarity
Matches 68; Conserv
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                                                                      ; Search time 28.9254 Seconds
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1 HAARMRTFMYWPSSVPVQPE......ESGDDPWVEHAKWFPRCEFL
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(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/FB_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-201-936-27
US-09-201-356-27
US-09-201-932-27
US-08-511-485-8
US-09-212-971-8
US-09-212-971-8
US-09-617-053A-8
US-09-617-053A-8
US-09-201-936-8
US-09-201-936-8
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US-09-201-932-8
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US-09-069-023-29
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US-09-212-971-14
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US-09-672-717-229
US-09-201-932-42
US-08-511-485-26
US-09-201-936-26
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                                          protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                    October 22, 2004, 11:08:12
                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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#### ALIGNMENTS

SEQUENCE 21, Application US/08511485

SEQUENCE 27, Application US/08511485

SEQUENCE 27, Application US/08511485

SEQUENCE 27, Application US/08511485

SEQUENCE 27, Application US/08511485

SEQUENCE 26

SEQUENCE 26

SEQUENCE 31

CONTANT: Baird, Stephen

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, TITLE OF INVENTION: MAMMALIAN IAP GENE CONTANT: Baird, Stephen

STATE: ADDITION: MAMMALIAN IAP GENE CONTANT: Baston

STATE: WAS CONTANT: USA

CONTANT: USA

CONTANT: USA

ZIP: 02110-2804

COMPUTER: READABLE FORM:
MEDICATION TYPE: Ploppy disk

COMPUTER: D4-10-2804

CONFUTER: D4-10-2804

CONFUTER: D4-10-2804

SOFTWARE: D4-10-10-2804

CLASSIFICATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 07540/00201

TELEFAX: 617/542-8070

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1 HAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60

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Gaps

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Length 68; Indels

ch 100.0%; Score 402; DB 2; 1 Similarity 100.0%; Pred. No. 9.1e-42; 68; Conservative 0; Mismatches 0; Gaps

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1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
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; Sequence 8, Application US/08511485
; Patent No. 5919912
; Patent No. 5919912
; APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenate, Aberander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAWMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROPES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-201-932-27

Sequence 27, Application US/09201932A

Sequence 27, Application US/09201932A

Sequence 27, Application US/09201932A

Relicant No. 666956A

APPLICANT: MacKenluk, Robert G.
APPLICANT: MacKenle, Alexander E.
APPLICANT: Daird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/00304

CURRENT APPLICATION NUMBER: US/09/201,932A

CURRENT APPLICATION NUMBER: US/09/201,932A

CURRENT APPLICATION NUMBER: PCT/1B96/01022

BARLIER PILING DATE: 1998-02-04

BARLIER PILING DATE: 1996-02-04

BARLIER PILING DATE: 1996-02-04

BARLIER PILING DATE: 1995-08-05

BARLIER PILING DATE: 1995-08-05

BARLIER PILING DATE: 1995-08-04

SARLIER PILING DATE: 1995-08-04

SARLIER PILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SEQUENCE: TARGET OF WINDOWS VERSION 4.0

SEQUENCE: ABSECT OF WINDOWS VERSION 4.0
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100.0%; Score 402; DB 4;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 68; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-09-201-932-27
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                        TYPE: PRT
ORGANISM: Homo sapiens
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                                                               ; ORGANISM: HO
US-09-011-356-27
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Matches 68; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Koreluk, Robert G.
APPLICANT: MacKenzle, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER APPLICATION NUMBER: 09/011,486
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
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US-09-201-936-27
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100.0%; Score 402; DB 3;
100.0%; Pred. No. 1.1e-40;
tive 0; Mismatches 0;
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SOFFWARE: FASTESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08800929A
Patent No. 6133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
                                                                                                              68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                 329 WFPRCEFL 336
          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                       61 WFPRCEFL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Com
OPERATING SYSTEM:
SOFTWARE: FastSEQ
                                                                                      Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
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               ; US-09-212-971-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-800-929A-8
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STATE:
                                                                         Query Match
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STATEMENT: MACKENZIE, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Eston, Peter
APPLICANT: Eston, Peter
APPLICANT: Frang, Benjamin K
APPLICANT: Pract, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: NUMBER: US/09/212,971B
CURRENT APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER PILING DATE: 1996-11-14
EARLIER PILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE FEASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
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                                                                                                                                                                                                SOFTWARE PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 07540/002001
TELEPROMONICATION NUMBER: 07540/002001
TELEPROMONICATION INFORMATION:
TELEPROMONICATION INFORMATION:
TELEPRAS: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 402; DB 2; Best Local Similarity 100.0%; Pred. No. 1.1e-40; Matches 68; Conservative 0; Mismatches 0;
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09212971B Patent No. 6107041
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-8
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    STREET: STREET: Boston
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                                                                                  USA
                                                                             COUNTRY:
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LENGTH: 618
TYPE: PRT
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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Tang, Benjamin K
APPLICANT: Tang, Benjamin K
APPLICANT: Pratt, Christine
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DEFECTION AND MODULATION OF
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                    0
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0
                                                                                          1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
                                                    Gaps
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Length 618;
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100.0%; Score 402; DB 3; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                 Indels
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Query Match
Best Local Similarity 100.
Matches 68; Conservative
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-201-936-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-09-672-717-223
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie Alexander E
APPLICANT: MacKenzie Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Pratt, Christine
ITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
ITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
ITLE OF INVENTION: DISEASE
ITLE OF INVENTION: UNBER: US/09/617,053A
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-13
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                               1 HAARMRIFWYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
    1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
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UG-09-201-936-8

Sequence 8, Application US/09201936

Sequence 8, Application US/09201936

GENERAL INFORMATION:
APPLICANT: MACKENIZE, ALEXANDER E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
ITILE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/03303

CURRENT FILINO DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 09/01/356

CURRENT FILING DATE: 1998-12-01

EARLIER APPLICATION NUMBER: 08/576,956

EARLIER PILING DATE: 1996-08-05

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-08-04

EARLIER PILING DATE: 1995-08-04

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-12-22

EARLIER PILING DATE: 1995-08-04

ENUMBER OF EQUINOS: 455

SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 402; DB 3;

Best Local Similarity 100.0%; Pred. No. 1.1e-40;

Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 618
                                                                                                                                                                                                                                                  Sequence 8, Application US/09617053A
Patent No. 6300492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
, ORGANISM: Homo sapiens
US-09-617-053A-8
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US-09-617-053A-8
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269 HAARMETFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 328
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Length 618;
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                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Korbert G.
APPLICANT: MacKenile, Robert G.
APPLICANT: MacKenile, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TILE OF INVENTION: PROBES, AND DETECTION METHODS
TILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT APPLICATION NUMBER: PCT/IB96/01022
EARLIER APPLICATION NUMBER: 08/51,485
EARLIER PILING DATE: 1995-08-05
EARLIER PILING DATE: 1995-08-04
EARLIER PILING DATE: 1995-08-04
SEALIER RELING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Lacasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antiense IAP Nucleic Acids and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025001
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100.0%; Pred. No. 1.1e-40;
iive 0; Mismatches 0;
  Query Match
100.0%; Score 402; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 68; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      US-09-011-356-8; Sequence 8, Application US/09011356A; Patent No. 6656704; GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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US-09-201-932-8
; Sequence 8, Application US/09201932A
; Sequence 8, Application US/09201932A
; Batent No. 6689562
; GENERAL INFORMATION:
    APPLICANT: Markenick, Alexander E.
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Baird, Stephen
    APPLICANT: Markenion, Peter
    ITILE OF INVENTION: PROBES, AND DETECTION METHODS
    FILE REFERENCE: 07891/003004
    CURRENT APPLICATION NUMBER: 09/011,356
    EARLIER APPLICATION NUMBER: 09/011,356
    EARLIER PELLING DATE: 1998-02-04
    EARLIER PELLING DATE: 1996-08-05
    EARLIER PELLING DATE: 1996-08-05
    EARLIER FILING DATE: 1995-08-04
    NUMBER OF SEQ ID NOS: 45
    SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                           Query Match
100.0%; Score 402; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 68; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/672,717
CURRENT FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 618
TYPE: PRT
CRGANISM: Homo sapiens
US-09-672-717-223
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GENERAL INFORMATION:
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US-09-201-932-8
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Best Local Similarity
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PCT-US95-05922A-2
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ADDRESSEE CORELLA, FYRER BAIN, CHIFTLAN,
ADDRESSEE CORELLA, FYRER BAIN, CHIFTLAN,
ADDRESSEE CORELLA, FYRER BAIN COLFIEINAN,
STREET, GENCRE FARM ROAD
STREET, GENCRETA BAIN COLFIEINAN,
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US-09-069-023-29
i Sequence 29, Application US/09069023A
j Patent No. 6348573
i GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
j APPLICANT: Nonez, Gabriel
j APPLICANT: Roseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
j SOFTWARE: Patentin Ver. 2.0
j SEQ ID NO 29
LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HAARMRITEMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
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97.8%; Score 393; DB 3; Length 618;
Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 67; Conservative 0; Mismatches 1; Indels
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Brazner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPAK: (415)791-1989
TELEPAK: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.59
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-09-069-023-29
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GenCore version 5.1.6
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October 22, 2004, 11:21:03; Search time 87.2836 Seconds (without alignments) 252.231 Million cell updates/sec 68 1 HAARMRIFMYWPSSVPVQPE......ESGDDPWVEHAKWFPRCEFL protein search, using sw model Gapop 10.0 , Gapext 0.5 US-09-654-743-27 **BLOSUM62** Perfect score: Scoring table: OM protein -Sequence: Run on:

Total number of hits satisfying chosen parameters: 1364641 segs, 323758627 residues Searched:

1364641

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

(cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
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(cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
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(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
Applications Published Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 27, Appl Sequence 27, Appl Sequence 8, Appli Sequence 223, Appli Sequence 223, Appli Sequence 2, Appli Sequence 2, Appli Sequence 338, Appli Sequence 338, Appli Sequence 348, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli
SUMMARIES	US-09-201-916-27 US-09-201-916-27 US-09-974-52-8 US-09-201-936-8 US-10-636-065-223 US-10-600-272-8 US-10-600-272-8 US-10-323-643-2 US-10-323-643-2 US-10-153-668-338 US-10-207-655-200 US-10-237-286-2 US-10-366-307-4 US-10-366-307-4 US-10-366-307-4 US-10-366-307-4
DB	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
% Query Match Length DB	688 618 618 618 618 618 618 618 618
% Query Match	100.0 100.0 100.0 100.0 100.0 97.8 97.8 97.8 97.8
Score	44444444466666666666666666666666666666
Result No.	1

	Sequence 78, Appl	Seguence 14, Appl	Somione 14, Appl	Seguence 42, Appl		Semience 36 April	Semience 26 April	Semience zo, Appi	_	a							, ້	7				Sequence 3, Appil	2 -	1 6	2 6	R	28	12	10	, ~	Sequence 29, Appl
m [	=	4	11S-09-201-936-42	n 9	0-600-272-42	36-26	9	9 US-09-974-592-6		14 US-10-232-286-4		14 US-10-366-307-6		US-10-600-272-6	16 US-10-730-476A-79	US-10-353-461-8	9 US-09-974-592-12	9 US-09-201-936-40	L6 US-10-636-065-227		115-10-232-286-9	L4 US-10-232-286-10	14 US-10-138-618-31		4 IIS-10-041-859-	0T_CCB_TE0 OT CD 71	Z/Z-009-01-00	4 US-10-041-859-12	US-1(	-10	.7 US-10-807-897-29
618	618	612	591	591	591	68	68	604	604	604	604	604	604	604	604	1140	009	602	602	602	48	48 1				9 4		7/1	268 1	280 1	280 1
97.8	91.0	91.0	89.6	89.6	9.68	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	80.6	79.1	79.1	79.1	70.4	67.2	62.2	58.2	58.2	2 2 2	0 0	20.0	28.5	57.7	57.7
393	366	366	360	360	360	340	340	340	340	340	340	340	340	340	340	340	324	318	318	318	283	270	250	234	234	234		100	234	232	232
14	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	CP	9 (	4. U.	44	<b>4</b> .5

#### ALIGNMENTS

APPLICANT: Moreluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Barrd, Stephen
APPLICANT: Barrd, Stephen
APPLICANT: Liston, Peter
ITILE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
ITILE OF INVENTION: MAMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER PILING DATE: 1998-02-04
EARLIER PILING DATE: 1998-02-04
EARLIER PILING DATE: 1995-12-2
EARLIER PILING DATE: 1995-12-2
EARLIER PELING DATE: 1995-12-2
EARLIER PILING DATE: 1995-08-05
EARLIER PILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FILING DATE: 1995-08-04 Sequence 27, Application US/09201936 Publication No. US20020187946A1 GENERAL INFORMATION: ORGANISM: Homo sapiens US-09-201-936-27 US-09-201-936-27 SEQ ID NO 27 TYPE: PRT

Gaps 0; Length 68; Indels 100.0%; Score 402; DB 9; 100.0%; Pred. No. 5.1e-39; iive 0; Mismatches 0; 68; Conservative Local Similarity Query Match Best Local S: Matches 68

09 1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWBSGDDPWVBHAK

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269 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVBHAK 328
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                                                                                                                                                        Length 618;
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APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holoik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09201936
; Sequence 8, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Kornelue, Robert G.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
                                                                                                                                                   ; Score 402; DB 9;
; Pred. No. 4.8e-38;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
BARLIER APPLICATION NUMBER: 09/011,356
BARLIER FILING DATE: 1998-02-04
BARLIER PELICATION NUMBER: PCT/IB96/01022
BARLIER APPLICATION NUMBER: 08/576,956
BARLIER PILING DATE: 1996-12-22
BARLIER APPLICATION NUMBER: 08/51,485
BARLIER APPLICATION NUMBER: 08/511,485
BARLIER RILING DATE: 1955-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 45 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 223, Application US/10636065; Publication No. US20040127694A1; GENERAL INFORMATION:
                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 68; Conservative 0;
; SEQ ID NO 8
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-592-8
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Matches 68; Conserv
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APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Isang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: DISTON, PRETERING
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: UNABER: US/09/974,592
CURRENT APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HAARMRTEMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
     1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
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Best Local Similarity 100.0%; Score 402; DB 16; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.1e-39;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NOLDELLE, KOUGL G.
APPLICANT: MACKENZIE, ALEXANDER E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/033006
CURRENT APPLICATION NUMBER: US 09/101,356
PRIOR APPLICATION NUMBER: PCT/IB96/01022
PRIOR FILING DATE: 1996-02-04
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1995-08-05
PRIOR FILING DATE: 1995-08-05
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ IO NOWBER: US 08/576,956
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ IO NOS: 45
NUMBER OF SEQ IO NOS: 45
SUFTWARE: FASELSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                           Sequence 27, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09974592 Patent No. US20020120121A1 GENERAL INFORMATION:
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US-10-600-272-27
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GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TILLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA; BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
             Publication No. US20030073159A1
                                                                                                                                                                                                                                           COUNTRY: USA
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US-10-323-643-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MacKentate, Alexander E.
APPLICANT: MacKentate, Alexander E.
APPLICANT: MacKentate, Stephen
APPLICANT: Liston, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
CURRENT APPLICATION NUMBER: US 09/011,356
PRIOR FILING DATE: 1996-02-04
PRIOR FILING DATE: 1996-02-05
PRIOR FILING DATE: 1996-02-05
PRIOR FILING DATE: 1996-08-05
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASTSEQ for Windows Version 4.0
                 FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10600272
Publication No. US20040157232A1
GENERAL INFORMATION:
Thereof
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Best Local Similarity 100.
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-636-065-223
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Best Local Similarity
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TITLE OF INVENTION:
                                                                                                                                                             SEQ ID NO 223
LENGTH: 618
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1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
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FUDIcation No. US200301085521
GENERAL INFORMATION:
THEORY FLOW Et al.
TILE OF INVENTION: Human Inhibitor of Apotosis Gene 1
TILE FEFERENCE: PF165F1D1
CURRENT APPLICATION NUMBER: US/10/323,643
CURRENT FILING DATE: 2002-12-20
FRIOR FILING DATE: 1995-06-05
FRIOR FILING DATE: 1995-06-05
FRIOR FILING DATE: 1995-06-11
NUMBER OF FO ID NOS: 10
SOFTWARE: Patentin version 3.1
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18.5 INCH DISKETTE
COMPUTER: 18.6 INCH DISKETTE
COMPUTER: 18.6 INCH DISKETTE
COMPUTER: 18.6 INCH DISKETTE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,588
FILING DATE: June 5, 1995
CLASSIFICATION 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/05922
FILING DATE: 11 MAY 1995
ATTOCNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                      325800-387
                                                                                                                                                                                                                                                                                                                                  NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 98.5
Matches 67; Conservative
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149 WFPRCEFL 156
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LENGTH: 438
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; Sequence 2, Application US/08464588

RESULT 7 US-08-464-588-2

WFPRCEFL 336

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STRANDEDNESS: single
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98.5%;
                 PatentIn version 3.0
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COMPUTER READABLE FORM:
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                                                                               TYPE: PRT ORGANISM: Homo sapiens
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Best Local Similarity
Matches 67; Conserv
NUMBER OF SEQ ID NOS:
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Best Local Similarity
Matches 67; Conserv
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                                                           LENGTH: 618
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                   SOFTWARE: Pat
SEQ ID NO 200
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Publication No. US20030118592A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-4011.
CURRENT APPLICATION VUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
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                                                                                                        1; Indels
                                                             Score 393; DB 14;
Pred. No. 3.8e-37;
0; Mismatches 1;
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Pred. No. 5.3e-37;
0; Mismatches 1
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VS-10-153-668-338
VS-10-153-668-338
Squence 338, Application US/10153668
Publication No. US20030092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: MATSUDA, Akio
APPLICANT: MIRAMATSU, Shuji
APPLICANT: SHIZAMA, Kenya
TILLE OF INVERTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HILE KEKEKENIE: 1.23-0.20.7.
CURRENT PEDLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,172
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-06-31
PRIOR FILING DATE: 2001-02-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-3313175
PRIOR APPLICATION NUMBER: JP 2001-30681
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-010
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PATENTIN VOY: 2.0
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98.5%;
                                                                  97.8%;
98.5%;
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Best Local Similarity 98.5
Matches 67; Conservative
                                                                Query Match
Best Local Similarity 98.5'
Matches 67; Conservative
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    ; ORGANISM: Homo sapiens
US-10-323-643-2
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US-10-207-655-200
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                                                                                       1 HAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVEHAK
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TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: PLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Sulte 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 618;
Length 618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 393; DB 14;
Pred. No. 5.3e-37;
Score 393; DB 14;
Pred. No. 5.3e-37;
0; Mismatches 1;
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brezner, David J.,774
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10232286 Publication No. US20030143579A1 GENERAL INFORMATION:
APPLICANT: Rothe, Mike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 618 amino acids
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INFORMATION FOR SEQ ID NO: 2:
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ATTORNEY/AGENT INFORMATION:
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Search completed: October 22, 2004, 11:37:10 Job time : 88.2836 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 98.5
les 67; Conservative
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Best Local Similarity 98.5
Matches 67; Conservative
                      329 WFPRCEFL 336
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ORGANISM: Homo sapiens
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US-10-260-708-63
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61 WFPRCEFL 68
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                                                                                      RESULT 14
US-10-260-708-63
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Best Local 8
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APPLICANT: Wooters, Joseph L
APPLICANT: Nickbarg, Bliott
APPLICANT: Oil, Yongchang
APPLICANT: Lin, Lih-Ling
TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
TITLE OF INVENTION: Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVEHAK
                                                                                                                                                                              APPLICANT: Reed, John C.

TITLE OF INVENTION: Methods for Determining the Prognosis

TITLE OF INVENTION: for Patients with a Prostate Neoplastic Condition
FILE REPERENCE: P-LJ 5659
CURRENT APPLICATION NUMBER: US/10/366,307
CURRENT APPLICATION NUMBER: US 60/356,956
PRIOR APPLICATION NUMBER: US 60/356,956
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVBHAK
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98.5%; Pred. No. 5.3e-37;
tive 0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/361,270
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/355,183
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PAtentin Ver. 2.1
                                                                                                                             ; Sequence 4, Application US/10366307; Publication No. US20030224399A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10361270 Publication No. US20040038299A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Conservative
                                     329 WFPRCEFL 336
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 67; Conserv
     61 WFPRCEFL
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LENGTH: 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Du, Chunying
APPLICANT: Yang, Qiheng
TITLE OF INVENTION: Method and Composition for Cleaving IAPS
FILE OF INVENTION: Method and Composition for Cleaving IAPS
FILE REPERENCE: 40716 (IP-022)
CURRENT APPLICATION NUMBER: US/10/730,476A
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin version 3.2
SEQ ID NO 78
LENGTH: 618
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Sequence 53, Application US/10260708
; Publication No. US20040063101A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Lee, Sang-Yull
; APPLICANT: Lee, Sang-Yull
; TITLE OF INVENTION: Human Sarcoma-Associated Antigens
; FILE REPRENCE: L00461/70138
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 63
; LENGIF 618
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98.5%; Pred. No. 5.3e-37;
live 0; Mismatches 1;
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GenCore version 5.1.6
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- protein search, using sw model OM protein

October 22, 2004, 11:08:02 Run on:

; Search time 23.8507 Seconds (without alignments) 274.320 Million cell updates/sec

US-09-654-743-27

Title: Perfect score:

1 HAARMRIFMYWPSSVPVQPE.....ESGDDPWVEHAKWFPRCEFL Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

inhibitor of apopt apoptosis-inhibiti kidhey inhibitor o inhibitor-of-apopt neuronal apoptosis neuronal apoptosis apoptosis inhibito apoptosis inhibito apoptosis inhibito apoptosis-inhibiti ORF MSV248 probabl cut17 protein - fi apoptosis inhibito apoptosis inhibito apoptosis inhibito probable apoptosis ORF MSV242 probabl IAP2 orf71 - Bomby valine-tRNA ligase valine tRNA synthe valine tRNA synthe apoptosis inhibito apoptosis inhibito apoptosis inhibito IAP1 orf27 - Bomby BIR repeat contain probable apoptosis Description SUMMARIES S68449 T10304 A53989 JC7568 A45679 A55478 T42628 S68452 S68450 JC5964 S69545 S69544 T10310 T28409 T31067 T03183 T43523 T30489 D36828 T41772 T37474 T30427 L28403 41814 Query Match Length DB 1447 496 497 497 275 150 286 292 4845 36.8 36.7 35.9 34.7 32.8 229.7 20.9 49.3 49.3 16.5 16.3 16.3 342 234 234 234 232 212 208.5 208.5 198 149 149 147.5 1139.5 1139.5 80.5 66.5 65.5 65.5 Result No. 

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2 C83782	2 T34179	L A39086	2 T02534	S24124	S57108	A96741	RGFFAL	E86449	T41644	148950	T06200	E89859	D96781	B49918	\$57961
423 2	306 2	2415 1	313 2	730 1	954 2	370 2	385 1	385 2	760 2	917 2	284 2	485 2	505 2	555 2	736 2
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64	63	62	61.5	60.5	60.5	9	09	09	9	9	59.5	59.5	59.5	59.5	59.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

H 03	KRSULT 1 S68450
1 10 0	apoptosis inhibitor hiap-2 - human Cispecies: Homo samiens (man)
	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 C;Accession: S68450
μχ	R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
K, K	A.Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP A.Reference number: A58182; MIID:96149249; PMID:8553191
A A	A.Accession: S68450
a a	A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
Ą	A;Residues: 1-618 <lls></lls>
∢ U	A;Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g118 C;Function:
Æ	A; Description: apoptotic suppressor
O E	C.Reywords: apoptosis; zinc finger
4	Fise / ell/Domain: King Hinger homology <rng></rng>
	Query Match 100.0%; Score 402; DB 2; Length 618; Best Local Similarity 100.0%; Pred. No. 5.8e-38; Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ø	FGCDGGLRCWESGDDPW
Δ	
O.	QY 61 WEPRCEFL 68
Ω	Db 329 WFPRCEFL 336
2	RESULT 2

JC5964

apoptosis inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: JC5964
R;Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem Biophys. Res. Commun. 243, 827-832, 1998
A;Reference number: JC5964; MUID:98162622; PMID:9501011
A;Stcossion: JC5564
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-358 <8TE>
A;Residues: 1-358 <8TE>
A;Cross-references: UNIPROT:062640; GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g29571'
F;307-351/Domain: RING finger homology <RRN>

Score 342; DB 2; Length 358; Pred. No. 2.3e-31; 85.1**%**; 82.4**%**; Query Match Best Local Similarity

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apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis viru apolytesis. Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Uul-2004 C;Datesion: A53989 R;Birnbaum, M.J.; Clem, R.J.; Miller, L.K. J. Virol. 68 2521-2528, 1994 A;Rirolam, M.J.; Clem, R.J.; Miller, L.K. J. Virol. 68 2521-2528, 1994 A;Reference number: A53989; MUID:94187094; PMID:8139034 A;Reference number: A53889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P41437; GB:L22564; NID:g456111; PIDN:AAB02610.1; PID:g456114 A;Note: authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology F;217-261/Domain: RING finger homology <RRN>
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C.comment: This protein, a new member of the inhibitor of apoptosis protein family, play
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.2%; Score 234; DB 2; Length 268; Best Local Similarity 53.7%; Pred. No. 3.4e-19; Matches 36; Conservative 13; Mismatches 18; Indels
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A,Map position: 20q13.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-268 <BIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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R.Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
A.P. Reference number: AS8182; MUID:96149249; PMID:8552191
A.R. Reference number: AS8182; MUID:96149249; PMID:8552191
A.R. Residues: Nature 379-370 A.S. Residues: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:AACS0371.1; PID:g118 C.; Ferwords: apoptoxis zinc finger
C.; Reywords: apoptoxis; zinc finger
C.; Reywords: apoptoxis; zinc finger
C.; Reywords: apoptoxis; zinc finger
F,553-597/Domain: RING finger homology <RNG>
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Best Local Similarity 83.8%; Pred. No. 6.5e-31;
Matches 57; Conservative 4; Mismatches 7;
      9
      Mismatches
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Best Local Similarity 53.78

- 36; Conservative
      Conservative
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WFPRCEYL 157
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172 YDRCEYV 178
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                     R; Yaraghi, Z.; Diez, E.; Gros, P.; MacKenzie, A.

Mamm. Genome 10, 761-763, 1999
A; Title: CDNA cloning and the S'genomic organization of Naip2, a candidate gene for muri
A; Reference number: Z22179; MUID:99315342; PMID:10384056
A; Status: preliminary; Lranslated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1447 < YAR>
A; Cross-references: UNIPROT:Q9QUK4; EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC7
A; Genetics:
A; Genetics:
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A;Residues: 1-36,'AT',37,'K',39,'L',41-44,'H',46-58,'Q',60-412,'A',414-427,'A',429-496
A;Cross-references: EMBL:U45881; NID:g1184313; PIDN:AAC46988.1; PID:g1184314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ARMRIFMYWPSSVPVQP-EQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAKW 61
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C.Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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C; Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
C; Keywords: apoptosis; zinc finger
F; 445-489/Domain: RING finger homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 208.5; DB 2;
Pred. No. 1.5e-15;
9; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.9%;
Best Local Similarity 53.7%;
Matches 36; Conservative
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271 SPKCQFV 277
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Best Local Similarity
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A.Residues: 1-275 <CRO>
A.Cross-references: UNTRROT:P41436; GB:L05494; NID:9289583; PIDN:AAA43835.1; PID:9289584
A.Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Go-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
Cispecies: No. 185478
RiRoy, N. Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; Baird, G. T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A.
Cell 80, 167-178, 1995
A;Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi
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A;Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A;Map position: Sq12-2-5q13
C;Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane ]
F;94-110/Domain: transmembrane #status predicted <TMAL>
F;470-477/Region: nucleotide-binding motif A (P-loop)
F;470-495(Domain: transmembrane #status predicted <TMML>
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F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A45679
R;Crook, N.E.; Clem. R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif. A;Accession: A45679; MUID:93188168; PMID:8445726
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 218; DB 2; Length 275; 50.7%; Pred. No. 2.3e-17;
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8; Mismatches 21; Indels
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55.2%;
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Best Local Similarity 55.2%
Matches 37, Conservative
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A;Residues: 1-1232 <ROY>
A;Cross-references: GB:U19251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 FDRCAYV 175
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apoptosis-inhibiting protein 1 - Orgyia pseudotsugata nuclear polyhedrosis virus c;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV c;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000 C;Accession: T10310 R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Bvans, J.; Harwood, S.; Rohrmann, G.F. Virology 229, 381-399, 1997 Virology 229, 381-399, 1997 Virology 229, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 381-399, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1997 Virology 220, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59040.1; PID:g1911287 C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology F;223-268/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.1%; Score 149; DB 2; Length 275; 38.8%; Pred. No. 1.7e-09; rative 12; Mismatches 29; Indels
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PNCNYI 83
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A; Residues: 1-497 and to fapotosis: Lefebvre, C:; Baird, S:; Cherton-Horvat, G:; Farahani, R; Liston, P:; Roy, N:; Tamai, K.; Lefebvre, C:; Baird, S:; Cherton-Horvat, G:; Farahani, R; Liston, P:; Roy, N:; Tamai, K.; Lefebvre, C:; Baird, S:; Cherton-Horvat, G:; Farahani, Nature 379; 349-353, 1996
A; Tible: Suppression of apoptosis in mammalian cells by NaIP and a related family of IAF A; Reference number: A58182; MUD:96149249; PMID:8552191
A; Reference number: A58182; MUD:96149249; PMID:8552191
A; Reference number: A58182; MUD:96149249; PMID:8552191
A; Residues: 1-161, C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 424-497 and A; Residues: 1-161, 'C', 163-422, 'Q', 4
C;Accession: 869545
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C BMBO J. 15, 2685-2694, 1996
BMBO J. 15, 2685-2694, 1996
BMBO J. 15, 2685-2694, 1996
A;Aritle: A conserved family of cellular genes related to the baculovirus iap gene and en A;Reference number: 869544; MUID:96256286; PMID:8654366
A;Accession: 869545
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-497 <DUC>
A;Cross-references: UNIPROT:Q24307; EMBL:UJ2373; NID:g1019116; PIDN:AAC47155.1; PID:g101
C;Genetics:
A;Gene: ilp
C;Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
F;446-490/Domain: RING finger homology <RRN>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O6-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69544; S68451
R;Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gilfillan, M.C
EMBO J. 15, 2685-2694, 1996
A;Title: A conserved family of cellular genes related to the baculovirus iap gene and expecience number: S69544; MUID:96256286; PMID:8654366
A;Accession: S69544
A;Statulus: preliminary; nucleic acid sequence not shown
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323 WYPGCKYL 330
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ORF MSV248 probable inhibitor of apoptosis protein (IAP) - Melanoplus sanguinipes entomo
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C;Date: 21-Vān-2000 #sequence_revision 21-Jān-2000 #text_change 09-Jul-2004
C;Date: 21-Jān-2000 #sequence_revision 21-Jān-2000 #text_change 09-Jul-2004
C;Accession: T28409
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28409
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C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D36828; C72853
R;Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D. Virology 191, 1003-1008, 1992
A;Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californic
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A;Reference number: A44221; MUID:93079853; PMID:1333113
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A; Accession: D36828
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Mesidues: 1-286 < CBRA>
A; Cross-references: UNIPROT: P41435; GB: S52569
A; Cross-references: UNIPROT: P41435; GB: S52569
A; Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A; Reference number: A72850; MUID: 94303173; PMID: 8030224
A; Reference number: A72850; MUID: 94303173; PMID: 8030224
A; Restreme DNA
A; Restreme DNA
A; Residues: 1199, 'L', 201-286 < ANR>
A; Residues: 1199, 'L', 201-286 < ANR>
A; Residues: 1199, 'L', viral apoptosis inhibitor IAP; RING finger homology
C; Superfamily: viral apoptosis inhibitor IAP; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ARMRTEM-YMPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAKW 61
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36.7%; Score 147.5; DB 2; Length 286;
Best Local Similarity 38.8%; Pred. No. 2.6e-09;
Matches 26; Conservative 14; Mismatches 26; Indels 1;
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193 NPQCYFV 199
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Search completed: October 22, 2004, 11:21:45 Job time: 24.8507 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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October 22, 2004, 10:50:26; Search time 128.896 Seconds (without alignments) 303:544 Million cell updates/sec protein search, using sw model OM protein -Run on:

US-09-654-743-27 Perfect score:

1 HAARMRTFMYWPSSVPVQPE......ESGDDPWVEHAKWFPRCEFL Sequence:

Scoring table:

1825181 seqs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q9YNL8 Q80SF4	IAP3 NPVOP	AAS01729	BIR7 HUMAN 071A73	080195	AAQ11158	Q6DBV7	Q81531 0968T8	Q8UWH2	07sxu1
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238 235	234 232	232	231 231	231	231	200	229	229	229
33	3.4 3.5	36	3 6	39	40	4 4 1 C	43	44	45

## ALIGNMENTS

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269 HAARMETFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                          Olimar-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
PRb-interacting protein RbBP-36.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            TISSUE=Lymph No.A.

TISSUE=Lymph No.A.

Fan Z.S., Ao S.Z.,

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

BEMBL, AF207599; AM73272.1; -.

RISSP; Q19065622; Cintracellular; IEA.

G0; G0:0005512; Fiprocein binding; IEA.

G0; G0:0005515; Fiprocein binding; IEA.

G0; G0:0006516; P: anti-apoptosis; IEA.

G0; G0:0006516; P: anti-apoptosis; IEA.

InterPro; IPR001370; BIR.

InterPro; IPR011029; DEATH like.

R InterPro; IPR011029; DEATH like.

R Pfam; PPG06619; CARD; 1.

SWART; SM0014; SIR; 3.

SWART; SM0014; SIR REPEAT 1; 3.

R PROSITE; PS01202; BIR REPEAT 2; 3.

R PROSITE; PS01202; BIR REPEAT 2; 3.

R PROSITE; PS01203; BIR REPEAT 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Score 393; DB 2; Length 534; 98.5%; Pred. No. 1.3e-37; 1.ve 0; Mismatches 1; Indels
       534 AA.
     PRT;
 PRELIMINARY;
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les 67; Conservative
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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BIR2\_HUMAN
BIR2\_HUMAN STANDARD; PRT; 618 AA. AC 013490; 016516;
DI 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update) 329 WFPRCEFL 336

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TISSUE-Testis, and Uterus;

XX TISSUE-Testis, and Uterus;

XX TISSUE-Testis, and Uterus;

XX Strausberg R.L., Feathgold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feathgold E.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B. Bucrow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

Asapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McWan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XIIlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glübs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhetriguez A.C., Grimwood J., Schwutz S.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;

Radinand and initial analysis of more than 15,000 full-length human
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-!- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts with TNF receptor associated factors 1 and 2 (TRAFI and TRAF2) to with TNF receptor receptor, which is then recruited to the tumor form an heteromeric complex, which is then recruited to the tumor necrosis factor receptor 2 (TNFR2).

-!- SUBUNIT: Interacts with SNAC and with PRSS25; these interactions inhibit apoptotic suppressor activity.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- TISSUE SPECIFICITY: Present in many fetal and adult tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.; "Suppression of apoptosis in mammalian cells by NAIP and a related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Fetal liver;
MEDLINE=96209843; PubMed=8643514;
WEDLINE=96209843; PubMed=8643514;
Uran A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
"Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors";
Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDINE=96128127; PubMed=8548810; MEDLINE=96128127; PubMed=8548810; MEDLINE=96128127; PubMed=8548810; Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.; Trothe ThFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
01-OCT-2004 (Rel. 45, Last annotation update)
Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99332054; PubMed=10404221;
Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
"Solution structure of a baculoviral inhibitor of apoptosis (IAP)
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                              protein 2) (IAP homolog B).
Name=BIRC2; Synonyms=API1, IAP2, MIHB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96149249; PubMed=8552191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
STRUCTURE BY NMR OF 266-363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family of IAP genes.";
Nature 379:349-353(1996).
                                                                                                                                                                                                                                                                                                                                                            to baculoviral inhibitor
Cell 83:1243-1252(1995).
                                                                                                                                    Homo sapiens (Human)
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protein 2)
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                    GO; GO:0004871; F:signal transducer activity; IEP.
GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
GO: GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Mainly expressed in adult skeletal muscle, thymus, testis, ovary, and pancreas, low or absent in brain and peripheral blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Score 393; DB 1; Length 618; 98.5%; Pred. No. 1.5e-37; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69899 MW; C1778D328063586D CRC64;
                                 -!- SIMILARITY: Belongs to the IAP family.
-!- SIMILARITY: Contains 3 BIR repeats.
-!- SIMILARITY: Contains 1 CARD domain.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. -> P (in Ref. 2
C. -> G (in Ref. 2
Q. -> L (in Ref. 2
L. -> W (in Ref. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UnterPro; IPR001370; BIR.
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR010181; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; CARD; 1.
Pfam; PF00619; Zf-C3HC4; 1.
SMART; SM00138; BIR; 3.
SMART; SM00138; BIR; 3.
SMART; SM00138; BIR; 3.
PROSITE; PS0143; BIR REPBAT_1; 3.
PROSITE; PS0143; BIR REPBAT_2; 3.
PROSITE; PS0109; ZF RING 1; PALSE NEG.
PROSITE; PS05089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARD.
                                                                                                                                                                          EMBL, L49431; AAC41942.1; -. EMBL, U45879; AAC50372.1; -. EMBL, U37547; AAC50508.1; -. EMBL, BC016474; AAH16174.1; -. EMBL, BC028578; AAH28578.1; -. PDB, 1QBH; NNR; A=263.363. Genew; HGNC:590; BIRC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 98.5 67; Conservative
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322
326
336
334
344
353
618 AA;
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259
453
308
1157
1157
1259
2269
301
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Best Local
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CONFLICT
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                      Genew; |
MIM; 60
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REPEAT
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DOMAIN
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1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK

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T and 2 genes.";

Genomics 46:495-503(1997).

Genomics 46:495-503(1997).

-!- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts with TNF receptor associated factors 1 and 2 (FRAF1 and TRAF2) to form an heteromeric complex, which is then recruited to the tumor corrections factor receptor 2 (TNFR2).

-!- SUBGINIT: Interacts with SMAC and with PRSS25; these interactions inhibit apoptotic suppressor activity (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- TISSUE SPECIFCITY: Expressed in heart, brain, spleen, lung, consistent of the LAP family.

-!- SIMILARITY: Contains 3 BIR repeats.

-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLITE=96128127; PubMed=8548810;
Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
"The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal muscle;
MEDLINE=98110590; PubMed=9441758;
Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
"Genomic characterization of the mouse inhibitor of apoptosis protein
                                                                                                                                                                                                                                                                                                                                                 MOUSE
BIR2 MOUSE
BIR2 MOUSE

0.2270; 008864;
01-N0V-1997 (Rel. 35, Last sequence update)
01-N0V-1997 (Rel. 44, Last sequence update)
05-VID-2004 (Rel. 44, Last annotation update)
05-VID-2004 (Rel. 44, Last annotation update)
05-VID-2004 (Rel. 44, Last annotation update)
05-VID-2004 (Rel. 44, Last annotation update)
05-VID-2004 (Rel. 44, Last sequence update)
05-VID-2004 (Rel. 44, Last sequence update)
06-VID-2004 (
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MGD; MG1:1197009; Birc3.

MGD; G0:0005515; P:procein binding; IPI.

InterPro; IPR001316; CARD.

InterPro; IPR001315; CARD.

InterPro; IPR001841; Znf.ring.

Pfam; PF00653; BIR; 3.

Pfam; PF00653; RIR; 3.

Pfam; PF00097; zf-C3HC4; 1.

SMART; SM00238; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (Se
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L49433; AAC42078.1; -.
EMBL; U88909; AAC53532.1; -.
                                                                                                                                                                                              329 WFPRCEFL 336
                                                                                                                           WFPRCEFL 68
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SEQUENCE FROM N.A.
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                                                                                                                           61
                                                                                                                                                                                                                                                                                                                 RESULT 3
BIR2 MOUSE
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A REDLINE=22388257; PubMed=12477932;

RA MEDLINE=22388257; PubMed=12477932;

RA Altascher R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altascher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altascher B.D., Collins F.S., Wagner L., Schaefer C.F., Bhat R.K.,

RA Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshivuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McEwan P.J., McKernan K.J., Malk V.J., Malker G.A., Gunaratue P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Plety J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Aoriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

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RA Jones S.J., Marra M.A.;

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RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

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RA Jones S.J., Marra M.A.;

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RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 HSARLRIFLYWPPSVPVQPEQLASAGFYYVDRNDDVKCFCCDGGLRCWEPGDDPWIEHAK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDFWVEHAK
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR_REPEAT_1; 3.
PROSITE; PS50209; BIR_REPEAT_2; 3.
PROSITE; PS50209; ZF_RING 1; FALSE_NEG.
PROSITE; PS50089; ZF_RING_2; 1.
Apoptosis; Direct protein sequencing; Repeat; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                    Score 366; DB 1; Length 61
Pred. No. 2.3e-34;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                               CARD.
RING-type.
E -> K (in Ref. 2).
; E08969D93C6C610D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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BIR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                     69676 MW;
                                                                                                                                                                                                                                                                                                                                                                       91.08;
                                                                                                                                                                                                                                                                                                                                                                                             88.28;
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27,
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                                                                                                                                                                                                                                                                                                                                                                                                               60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 WFPRCEFL 329
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                                                                                                                                                                                                                                                                      565
380
612 AA;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 WFPRCEFL
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CONFLICT
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REPEAT
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                                                                                                                                                                                                                                             DOMAIN
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RESULT 6
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TISSUE=Prostate;

MEDILINE=22388257; PubMed=12477932;

MEDILINE=22388257; PubMed=12477932;

MEDILINE=22388257; PubMed=12477932;

Altschul S.P., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A placcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B. Darcherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaranne P.H.,
R.A Bosak S.A., McEwan P.J., Workernan R.J., Madan A., Gay L.J., Hulyk S.W.,
R.A Helton B.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R.A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A., Schmutz J., Myers R.M., Butterfield Y.S.,
R.A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A righniski M.I., Skalska U., Smailus D.E., Schnerch A., Schnein J.E.,
A granner and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 589 AA; 66846 MW; 526BCBAA9052EF49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526ECBAA9052EF49 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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89.3%; Score 359; DB 2; Le
Best Local Similarity

88.2%; Pred. No. 1.4e-33;

Matches

60; Conservative

3; Mismatches

5;
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InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SWART; SW00238; BIR; 3.
SWART; SW00144; CARD; 1.
SWART; SW01149; RING; 1.
SWART; SW01143; BIR REPEAT_1; 3.
PROSITE; PS501282; BIR REPEAT_2; 3.
PROSITE; PS501282; BIR REPEAT_2; 3.
PROSITE; PS501809; CARD; 1.
Metal-binding; Zinc; Zinc; Zinc; Zinc; SEDC SEQUENCE 589 AA; 66846 MW; 526BC
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02-MAR-2004 (TṛEMBLrel. 27,
02-MAR-2004 (TṛEMBLrel. 27,
02-MAR-2004 (TṛEMBLrel. 27,
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AAH62055
ID AAH62056
AC AAH6
DT 02-M
DT 02-M
DT 02-M
DT 02-M
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Score 359; DB 2; Length 589;

89.38;

Query Match

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDINE=2200588; PubMed=12023884;
MEDINE=2200588; PubMed=12023884;
Dong Z., Nishiyama J., Yi X., Venkatachalam M.A., Denton M., Gu S.,
Li S., Qiang M.,
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GO; GO:0005515; F:protein binding; IEA.
GO; GO:000842; F:ubiquitin.protein ligase activity; IEA.
GO; GO:0008270; F:ubiquitin-protein ligase activity; IEA.
GO; GO:00068216; F:arinc ion binding; IEA.
GO; GO:0006816; P:arti-apoptosis; IEA.
GO; GO:0042881; P:regulation of apoptosis; IEA.
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SMART; SM00114; CARD; 1.
SNART; SM00118; CARD; 1.
SNOSITE; PS01282; BIR REPEAT 1; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS50209; ZRNING 2; 1.
Metal-binding; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc; Zinc
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-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF190020; AAF04585.1; --
HSSP; Q13490; 1QBH.
88.2%; Pred. No. 1.4e-33; ive 3; Mismatches 5;
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InterPro; IPR001375; BIR.
InterPro; IPR011029; DEATH like.
InterPro; IPR011029; Znf_ring.
Pfam; PP00653; BIR; 3.
Pfam; PP00619; ZARD; 1.
Pfam; PP00619; Zf_C3HC4; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 86.87
    Best Local Similarity 88.2<sup>3</sup>
Matches 60; Conservative
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176 WFPRCEYL 183
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NCBI_TaxID=9031;
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RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;

T. "Cloning and characterization of the rat homologues of the Inhibitor of Apoptosis protein 1, 2, and 3 genes.";

RI BMC Genomics 3:5-5(2002).

C. -! SIMILARITY: Contains 1 RING-type zinc finger.

BMC Genomics 3:5-5(2002).

C. -! SIMILARITY: Contains 1 RING-type zinc finger.

BMC Genomics 3:5-5(2002).

C. -! Contains 1 RING-type zinc finger.

BMC Genomics 3:5-5(2002).

BMC Genomics 3:5-5(2002).

C. -! Cubiquitin ligase complex; IEA.

BMC GO: 00006151; Cubiquitin ligase activity; IEA.

BMC GO: 00006210; F: protein binding; IEA.

BMC GO: 00006210; F: protein binding; IEA.

BMC GO: 00006210; F: protein ubiquitination; IEA.

BMC GO: 00006210; P: protein ubiquitination; IEA.

BMC GO: 00006210; P: protein ubiquitination; IEA.

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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Inhibitor of apoptosis 1 (Fragment).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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86.8%; Pred. No. 7.3e-33;
ative 3; Mismatches 6; Indels
                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Inhibitor of apoptosis protein 2.
                                                                                    589 AA
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Best Local Similarity 86.89
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NCBI_TaxID=9031;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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STRAIN=breed Leghorn, TISSUE=Spleen,
MEDLINE=21158006, PubMed=11261557,
Zhou H., Liu W., Lamont S.J.;
Thou H., Liu W., Lamont S.J.;
Thou H., Liu W., Lamont S.J.;
Thou H., Sin William and Chicken lines and mammalian species in specific genes.";
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MEDLINE=21158006; PubMed=11261557;

A Zhou H., Liu W., Lamont S.J.;

T "Genetic variation among chicken lines and mammalian species in specific genes";

Poult. Sci. 80:284-288 (2001).

R EMBL; AF221083; AAF35320.1; -

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005612; P:anti-apoptosis; IEA.

R InterPro; IPR001370; BIR.

R Ffam; PF00653; BIR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.3%; Score 351; DB 2; Length 197;
82.4%; Pred. No. 3.9e-33;
tive 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22602 MW; D7923DABCF623E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEWBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TW-2003 (TrEMBLrel. 24, Last annotation update)
Inhibitor of apoptosis I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.3%; Score 351; DB 2;
Best Local Similarity 82.4%; Pred. No. 3.9e-33;
Matches 56; Conservative 7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AA.
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                                                                                                                                                                                                                                                                                                                      -: TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in both cortical and medullary cells of the thymus. Expressed at relatively high levels also in spleen, bursa, intestine and lung and at very low levels in testis, brain and skeletal muscle.
-: INDUCTION: High levels are induced within 4-8 hours of T-cell activation in spleen and thymus.
-: DOMAIN: The ring finger is important for its antiapoptotic effect.
-: SIMILARITY: Belongs to the IAPP family.
-: SIMILARITY: Contains 1 RARD domain.
-: SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                T cell apoptosis
                                                                                                                                                                                                                                                             Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W., "ITA, a vertebrate homologue of IAP that is expressed in T
                                                                            BIR_CHICK STANDARD; PRT; 611 AA.
090660; 057319;
01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
05-UTU-21097 (Rel. 44, Last annotation update)
Inhibitor of apoptosis protein (IAP) (Inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00518; ZF RING 1; FALSE NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q13490; 1QBH.
INTERFEVO; IPROQ1370; BIR.
INTERPFVO; IPROQ1315; CARD.
INTERPFVO; IPROQ11029; DEATH like.
INTERPFVO; IPROQ1841; ZNE_ring.
Pfam; PPOO653; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGU; PF00097; ZF-C3HC4; 1.
PROSITE: PS01282; BIR REPEAT 1; 3.
PROSITE: PS50143; BIR REPEAT_2; 3.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                             TISSUE=Spleen;
MEDLINE=97101112; PubMed=8945639;
                                                                                                                                                                                                                                                                                                 DNA Cell Biol. 15:981-988(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U27466; AAB48118.1; ".
EMBL; AF008592; AAB88044.1; -.
                                                                                                                                                 protein).
Name=ITA; Synonyms=IAP1;
                                                                                                                                                                   Gallus gallus (Chicken)
                     177 WFPRCEYL 184
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
    WFPRCEFL
                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                        to Ref.
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    61
                                                                                                                                                protein)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HAARMRIFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 351; DB 1; Length 611; Pred. No. 1.3e-32;
                                                                                                                                                                                                                                                                       2)
             242 BIR 1.
242 BIR 2.
329 BIR 3.
326 CARD.
599 RING-type.
27 F -> L (in Ref. 2).
150 R -> Q (in Ref. 2).
163 S -> F (in Ref. 2).
183 S -> F (in Ref. 2).
192 CLW -> FLS (in Ref. 2).
203 DD -> YY (in Ref. 2).
214 VN -> CQ (in Ref. 2).
215 WNSSCT -> EQLLS (in Ref. 2).
216 WN -> YY (in Ref. 2).
217 VN -> GQ (in Ref. 2).
218 WNSSCT -> EQLLS (in Ref. 2).
219 VN -> GQ (in Ref. 2).
210 VN -> GQ (in Ref. 2).
211 VN -> GQ (in Ref. 2).
212 VN -> CQ (in Ref. 2).
213 WNSSCT -> EQLLS (in Ref. 2).
214 VN -> GQ (in Ref. 2).
215 K -> C (in Ref. 2).
216 C -> C (in Ref. 2).
217 -> C (in Ref. 2).
218 C -> C (in Ref. 2).
219 C -> C (in Ref. 2).
210 C -> C (in Ref. 2).
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...a 5; Indels
Repeat; Zinc-finger.
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15-DEC-1998 (Rel. 37, Last sequence update)
05-UDC-2004 (Rel. 44, Last annotation update)
putative inhibitor of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98162622; PubMed=9501011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U79142; AAC39171.1; -. PIR; JC5964; JC5964.
                                                                                                                                                                                                                                                                                                                                                                                                                    87.3%;
protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                    242
3329
3236
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44026
4906
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                                                                                                                                                                                                                                                                                                                                                                                       611 AA;
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     Nuclear
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Sus scrofa (Pig).
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                                      PIAP_PIG
ID _PIAP_PIG
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                                    REPEAT
REPEAT
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90 YAARFKIFCNWPSSIPVHPBQLASAGFYYMGHSDDVKCFCCDGGLRCWBSGDDPWVEHAK 149
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                   1 HAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=96128127; PubMed=8548810;

Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;

"The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96149249; PubMed=8552191;
Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
"Suppression of apoptosis in mammalian cells by NAIP and a related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal liver;
MEDLINE=96209843; PubMed=8643514;
Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
"Cloning and expression of apoptosis inhibitory protein homologs that
                                                                                                                                                                                                                                                                                                                                                                                                            Q13489; Q16628; QPHC27; Q9UP46;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
protein 1) (HIAP1) (HIAP-1) (C-IAP2) (TNFR2-TRAF signaling complex
protein 1) (IAP homolog C) (Apoptosis inhibitor 2) (API2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                                                                                                                                                                                            Score 342; DB 1; Length 358;
Pred. No. 8.5e-32;
                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                             311 346 RING-type.
358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;
                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                  PROSITE; PS50209; CARD; 1. PROSITE; PS00518; ZF_RING_1; FALSE_NEG.PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=BIRC3; Synonyms=API2, IAP1, MIHC;
       InterPro: IPR001370; BIR.
InterPro: IPR001315; CARD.
InterPro: IPR001315; CARD.
InterPro: IPR001029; DEATH like.
InterPro: IPR0010841; Znf ring.
Pfam; PF00653; BIR; 2.
Pfam; PF006519; ZnRD; 1.
Pfam; PF006719; ZnRD; 1.
Pfam; PF00097; zf-C3RC4; 1.
SMART; SM00128; BIR; 2.
SMART; SM00114; CARD; 1.
PROSITE; PS01282; BIR REPEAT 1; 2.
PROSITE; PS01282; BIR REPEAT 2; 2.
PROSITE; PS01029; CARD; 1.
                                                                                                                                                                             BIR 1.
BIR 2.
CARD.
                                                                                                                                                                   Apoptosis, Repeat, Zinc-finger
                                                                                                                                                                                                                                           85.1%;
82.4%;
                                                                                                                                                                                                                                                                 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family of IAP genes.";
Nature 379:349-353(1996).
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                150 WFPRCEYL 157
                                                                                                                                                                                                                                                                                                                             61 WFPRCEFL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                      Best Local Similarity
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R. Muncion to inhibit apoptosis and/or bind tumor necrosis factor RE function to inhibit apoptosis and/or bind tumor necrosis factor and an electronic associated & Geicorg.";

R. MUNCES SERON NA. M. Pontili R. D. N. 914974-4978 [1956].

R. MINISTERSPENDEN A.J. Fontili R. D. N. M. Zonneveld A.J., de Vries C.J., R. M. Marchen A.J. Fontili R. D. N. M. Zonneveld A.J., de Vries C.J., R. Wascular endothelial genes that are responsive to tumor necrosis RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed in atherseciartic lesions, RT factor-alpha invitro are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions and are expressed and solutions are proposed and are expressed and solutions and are expected and are expressed and solutions are proposed and are expressed and solutions and are expected and are expressed and solutions and are expected and are expressed and solutions and are expected and are expressed and solutions and are expected and are expressed and solutions and are expressed and solutions and are expected as a solution and are expressed and solutions are are expressed and solutions and are expected as
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NCBI_TaxID=8355;
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                                                                                                                                             initiative.
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                                                                                                                                                                                                                 GO: GO:0005515; F:protein binding; NAS.
GO: GO:0006916; P:anti-apoptosis; TAS.
GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Cranīata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RING-type.
BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N -> Y (in Ref. 4).
N -> H (in Ref. 2).
H -> E (in Ref. 2).
A -> P (in Ref. 2).
A -> P (in Ref. 2).
F -> L (in Ref. 2).
F -> L (in Ref. 2).
C -> P (in Ref. 2).
W, B581A00BA9AAB4A7 CRC64;
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       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01282; BIR REPEAT 1; 3.
PROSITE; PS50143; BIR REPEAT 2; 3.
PROSITE; PS50209; CARD; 1.
PROSITE; PS500509; ZF RING 1; FALSE NEG.
PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last seque
01-0CT-2004 (TrEMBLrel. 28, Last annot
19pothetical protein.
Xenopus laevis (African clawed frog).
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BIR 2.
BIR 3.
CARD.
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InterPro; IPR001370; BIR.
InterPro; IPR0011039; DARTH 11ke.
InterPro; IPR001841; Znf_ring.
Pfam; PP00653; BIR; 3.
Pfam; PP00619; ZARD; 1.
Pfam; PP00097; Zf-C3HC4; 1.
SWART; SM00124; BIR; 3.
SWART; SM00184; RING; 1.
                                     EMBL; L49432; AAC41943.1; -.
EMBL; U45878; AAC50371.1; -.
EMBL; U37546; AAC50507.1; -.
EMBL; AF070674; AAC8332.1; -.
EMBL; BC037420; AAH37420.1; -.
EMBL; AF178945; AAG09369.1; -.
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ilarity 83.8%;
Conservative
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PIR, S68449, S68449.
HSSP, Q13490, 1QBH.
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552 5
604 AA;
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Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapieton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapieton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roberts S.A., McEwan D.J., McKernan K.J., Malzk J.A., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards J., Helton E., Kettemen M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raparsley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raparsley R.W., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Sahintz J., Myers R.M., Butterfield Y.S.,

Raparsley R.W., Touchman A., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryd Miniting M. Main A. W. Schmutz J., Myers R.M., Butterfield Y.S.,

Ryd Miniting M. M. Salska U., Sanints D.E., Schnerch A., Schein J.E.,

Ryd Monse S.J., Marra M.A.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes;
                                    TISSUE=Embryo;

BEDLINE=22341132; PubMed=12454917;

Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                               "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC077368; AAH77368.1; -.
Hypothetical protein:
SEQUENCE 604 AA; 68551 MW; 78B5CC51E111CC84 CRC64;
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Last annotation update)
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80.6%; Pred. No. 1.3e-30;
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SEQUENCE FROM N.A.
MEDLINE=20373792; PubMed=10917738;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391(2002).
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Matches 54; Conservative
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NCBI_TaxID=7955;
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SEQUENCE FROM N.A.
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PubMed=12477932;
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Search completed: October 22, 2004, 11:20:54 Job time: 129.896 secs
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Inohara N., Numez G., "Genes with homology to mammalian apoptosis regulators identified in zebrafish."; Cell Death Differ. 7:509-510(2000).
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TremBrancel. 26, Last annotation update)
101-MAR-2004 (Zebrafish) (Danio rerio).
102-2004 Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
102-2007 Mctinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
103-2007 Mctinopterygii; Teleostei; Ostariophysi; Cypriniformes;
103-2007 Mctinopterygii; Metazoa, Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii; Mctinopterygii
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R HSSI, Q13490, 1QBH.

R GO; GO:000151; C:ubiquitin ligase complex; IEA.

GO; GO:0004815; F:protein binding; IEA.

R GO; GO:0004815; F:protein binding; IEA.

R GO; GO:00048216; F:zinc ion binding; IEA.

R GO; GO:00045567; P:zinc ion binding; IEA.

R GO; GO:00045667; P:protein ubiquitination; IEA.

R GO; GO:0015567; P:protein ubiquitination; IEA.

R GO; GO:0042981; P:regulation of apoptosis; IEA.

R GO; GO:0015567; P:protein ubiquitination; IEA.

R GO; GO:0015567; P:protein ubiquitination; IEA.

R GO; GO:0015657; P:protein ubiquitination; IEA.

R InterPro; IPR0011029; DBATH like.

R InterPro; IPR0011029; DBATH like.

R InterPro; IPR001189; DBATH like.

R Pfam; PF00653; BIR; 3.

Pfam; PF00653; BIR; 3.

R Pfam; PF00619; CARD; 1.

R SWART; SW00114; CARD; 1.

R RAWART; SW00114; CARD; 1.

R R PROSITE; PS50143; BIR REPEAT 1; UNKNOWN 2.

R R PROSITE; PS50143; BIR REPEAT 2; 3.

R R PROSITE; PS50199; ZRRING 2; 1.

M Metal binding; Zainc-finger.

SEQUENCE 628 AA; 70098 MW; 5B68CEB6AB7C8A95 CRC64;
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83.1%; Pred. No. 1.3e-30;
iive 6; Mismatches 5; Indels
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-1- SIMILARITY: Contains I RING-type zinc finger.
EMBL; AY247786; AAR04483.1; -
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008210; F:zinc ion binding; IEA.
                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
Inohara N., Nunez G.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AF442200; AAL33679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 AA.
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les 54; Conservative
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          RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RATARA RA
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4 RMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFGCDGGLRCWESGDDPWVEHAKWFP 63
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GO; GO:0016567; P:Protein ubiquitination; IEA.

GO; GO:0042981; P:regulation of apoptosis; IEA.

R InterPro; IPR001315; CARD.

R InterPro; IPR001841; ZnE ring.

R Pfan; PF00065; BIR; 3.

R Pfan; PF00065; BIR; 3.

R Pfan; PF00097; zf-C3HC4; 1.

R SMART; SM00114; CARD; 1.

R SMART; SM00114; CARD; 1.

R RAPR; SM0114; CARD; 1.

R PROSITE; PS501282; BIR REPEAT 1; UNKNOWN 2.

R PROSITE; PS501282; BIR REPEAT 2; 3.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.

R PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.1%; Score 334; DB 2; Length 64
83.1%; Pred. No. 1.4e-30;
ive 6; Mismatches 5; Indels
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les 54; Conservative
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